

[illegible]

Db	1158	AAAACTCTTCAGAGTCGATTCTATAGACAGATTTTGAAGACAGAGAGAACACAGAGAGAGAGT	1217
Qy	302	AsnLeuAspGluGluValAsnValIleProProHisIleProValIardGluValMetAsn	321
Db	1218	AAATTTTAAAGAAAGAGGAAAGGAAATGTCACACATCTCAGTTAGGACACTGTATAGAAC	1277
Qy	322	ThrIleGluGluLeuMetMetIleLeuAsuSerAlaSerAspIleProIleLeuLeuLeu	341
Db	1278	ACATCCCAACAAATTAATGATGATTTTAAATTCAGCAAGTGAICCAACCTTCACAAAAATCG	1337
Qy	342	IleSerTyrPheAsnAspCysThrValAsnProLysGluSerIleLeuLysAlaValLys	361
Db	1338	ATTTCTTATTTTAAACAACTGCACATGAAATCCAAAGAAAGATATACTCGAAAGACAGAG	1497
Qy	362	AspIleLysMetIlePhePheLysPheAlaLysAlaValCysGluGluCysValGlu	381
Db	1398	GATATAGATACATCTTAAAGAGAAATTTGCTAAAGTGTGGAGACAGGGTTGGTGTGAA	1457
Qy	382	IleGlySerGluArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMet	401
Db	1458	ATTTCGATCAGAGCATACAAACTTTCAGTTCCTCTCTATACCCAGTAAAGCAAACGATG	1517
Qy	402	LeuLysSerGluGluAlaArgLeuSerIleGluAspPheSerLysLeuLeuAsnAspAsn	421
Db	1518	CTTAAATCAGAGAGAGAGAGATTAATCCATTCAAAATTTTAGCAAACTTCTGAAATGACAGC	1577
Qy	422	IlePheHisMetSerLeuLeuAlaCysAlaLeuGluValIleMetAlaThrTyrSerArg	441
Db	1578	ATTTTTCATATATCTTATTGGCTGGCGTCTTAGGGTTGTAAATGGACACATATAGACAA	1637
Qy	442	SerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPheProTyrIleLeuAsnVal	461
Db	1638	AGTACTGTCAGAAATGATGATGTCGAAACAGATATCTCTTCCCATCGAATGTCAATGTCG	1697
Qy	462	LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly	481
Db	1698	CTTAAATTAAGAAAGCTTGAATTTTACAAAGTGATGAAAGTTTATCAAAATAGAAAGGC	1757
Qy	482	AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSer	501
Db	1758	AACTTGCAGAGAGAAATGATAAACAATTTAGAACCATGTGAACATCGAATCATGGAATCG	1817
Qy	502	LeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGluSerLysAspArgGlu	521
Db	1818	CTTCCATGGCTCCACATTCACCTTATTTCAGATCTTAATCAACATCAAAAGCCAGCAA	1877
Qy	522	GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGluHisAsnHis	541
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Qy	542	ThrAlaAlaSerMetTyrLeuSerProValArgSerProLysIleLysGlySerThrThr	561
Db	1938	ACTGACCAATATATATATTTTCTCTGAAATCTCAAGAGAAAAAAGGTTCAACTATG	1997
Qy	562	ArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAlaPheGluThrGluLys	581
Db	1998	CGTCTAAATTCCTACTCCAAATTCAGAGACAAAGCAACCTCAGGCTTCCACACCCCAAG	2057
Qy	582	ProLeuIleSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeu	601
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Qy	602	ArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIle	621
Db	2118	CGGCTAAATATACATTGTGAAGGCTCTGCTGAGACACCCAGAAATTAGAACATATATAT	2177
Qy	622	TrpThrLeuPheGluHisThrLeuGluHisGluIyrGluLeuMetArgAspArgHisLeu	641
Db	2178	TGACCCCTTTTCAGACACACCTTCAGAAATCAGATATCAACTCATCAGACAGACGCAATTC	2237
Qy	642	AspAlaIleMetMetLeuSerMetTyrGlyIleLysValLysAsnIleAspLeuLys	661

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10 2248 GATCAAAATACATGCTGTAAGTATGAGTAAAGTAAATACACCTTAA 2297
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38 2658 ATTCTGAAATTTCCAAATAATATATATATATATATATATATATATATATATATATAT 2717
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44 822 GlySerAspGlnAlaAspGlnLysLysIleLeuProGlnLysIleSerLysPheGlnGln 841
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46 2778 GATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2837
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48 842 LeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 861
49
50 2838 CTGGTAAATATATATATATATATATATATATATATATATATATATATATATATATAT 2897
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52 862 AspThrSerAsnLysGlnGlnLys 869
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54 2898 CATATCTTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2941
55

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RESULT 10
AR144797
DEFINITION Sequence 7 from patent US 6210939.
ACCESSION AR144797
VERSION AR144797.1 GI:1106664
KEYWORDS
SOURCE
ORGANISM

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REFERENCE 1 (bases 1 to 2995)
AUTHORS Greeny,R.J., Willis,K.N. and Maneval,D.C.
TITLE Recombinant adenoviral vector and methods of use
JOURNAL Patent: US 6210939 A 7 Oct 2000
FEATURES
Location/Qualifiers
1..2995
/organism "unknown"

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BASE COUNT 975 a 613 c 593 g 810 t
GAGGAG

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Alignment Scores:
Prod. No.: 5,186-411 Length: 2995
Score: 4444.50 Matches: 866
Percent Similarity: 93.4% Conservative: 1
Best Local Similarity: 93.4% Mismatches: 2
Query Match: 98.72% Indels: 59
DB: 6 Gaps: 1

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QY 21 ProAlaProProProProProProProProProProProProProProProProPro 40
DB 199 CCGGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 258
QY 41 AspLeuProLeuValArgLeuGlnPheGlnIleThrGlnIleProAspPheThrAlaLeu 60
DB 259 GACCTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 318
QY 61 CysGlnLysLeuLysIleProAspHisValArgLeuArgAlaAlaAlaAlaAlaAlaAla 80
DB 319 TGTGAGAAATTAAGATACCAATCACTGACAGACAGCTTGGTAACTTGGAGAAA 378
QY 81 ValSerSerValAspGlyValLeuGlyCysIleThrIleCysLysLysLysLysLysLys 100
DB 379 GTTTCATCTGTGGATGGATGATGAGAGGTATATATTCAAAAGAAAAAGAACTGTGGGAA 438
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DB 439 ATCTGATATCTTTATGAGCAGCTTGCATGACATGACATGACATGACATGACATGACATG 498
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DB 499 CAGAAAAACATAGAAAACAGTGTGTAAGATGATGTAAGATGATGTAAGATGATGTAAGAT 558
QY 141 SerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysLysLysLysLysLys 160
DB 559 AGTACAAAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
QY 161 LeuPheSerLysLeuGlnAArgIleCysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 180
DB 619 CTCTTCTGCTAAATTTGAGAACTATGATGATGATGATGATGATGATGATGATGATGATGAT 678
QY 181 Met
DB 679 ATATCTACTGAGAAATATAATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
QY 181
DB 739 GCTAAGGGGAAGTATTACAAATGGAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 798
QY 181
DB 799 TCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 858
QY 182 ValAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSer 201
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QY 202 AlaArgIleAlaLysGlnLeuGlnAspIleArgIleIleIleGlnLeuLeuLeuLysGln 221
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QY 282 LysThrLeuGlnThrAspSerIleAspSerPheGlnIleThrGlnArgThrProArgLysSer 401
DB

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07 302 AsnLeuAspGluGluValAsnValIleProProHisThrProValArgThrValMetAsn 321
11 1162 ANAGTGTATGAGAGGTAAGAGTGTGTACTGCAACACTCCGCTTATGAGATGATGAT 1420
07 322 ThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 341
18 1221 AATATTCACCAATTAATTCGGTCAATTTAAATTCCTGCAAGTCAATCAGCCATCAGAAAATCTG 1280
07 342 IleSerTyrPheAsnAsnCysThrValAsnProLysGlnSerIleLeuSerValValLys 361
18 1281 ATTTCGATTCATTAATATGCAAGTCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1340
07 362 AspIleGlyIleThrPheGlyGlnGlySerPheAlaLysAlaValIleGlyGlyCysValGlu 381
18 1441 GATGTTCGACATCTTTAAAGCAATTTGCTTAAGCTGTGAGCTGTGAGCTGTGAGCTGTGAG 1400
07 382 IleGlySerGlnAlaArgTyrLysValArgLeuTyrTyrArgValMetGluSerMet 401
18 1401 ATGCGATATCAGGATATAAACTTGGAGTGGGATGTGATACCGTGTGCAAGCAATCCCATG 1460
07 402 LeuLysSerGlnIleGlnAlaLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsn 421
11 1401 GTTAAATCAG 1520
07 422 IlePheHisMetSerLeuLeuAlaCysAlaLeuGluValIleMetAlaThrIleTyrSerArg 441
18 1521 AGCTTCATATGCTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1580
07 442 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProThrIleLeuAsnVal 461
18 1581 AGTATATCAGGATATTCATCTGATCAACAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1640
07 462 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGlnSerPheIleLysAlaGluGly 481
18 1641 GTTAAATTAAG 1700
07 482 AsnLeuThrArgGluMetIleLysHisIleGluArgCysGluHisArgIleMetGluSer 501
18 1701 AATTTGACAG 1760
07 502 LeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 521
18 1761 GTTCAAG 1820
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18 1821 GGAAGCTTGAAG 1880
07 542 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysGlySerThrThr 561
18 1881 ACTGAG 1940
07 562 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 581
18 1941 GAGGAG 1997
07 582 ProLeuLysSerThrSerLeuSerLeuPheTyrLysValTyrArgLeuAlaTyrLeu 601
18 1998 GATTCGAG 2057
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18 2058 GGAATTAATACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2117
07 622 TrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgIleLeu 641
18 2118 GGCAGATGCTTCAGGATATCAGGATATCAGGATATCAGGATATCAGGATATCAGGATATCAGG 2177
07 642 AsnIleIleMetMetCysSerMetTyrGlyIleCysLeuValTyrLysAlaLeuAspLeuLys 661
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Search completed: January 18, 2003, 22:30:20
Job time : 3906.22 secs

[illegible]


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RESULT 2

AAV54991

ID AAV54991 standard; DNA: 3218 BP.

XX AAV54991;

AC AAV54991;

XX 26-NOV-1998 (first entry)

XX DNA sequence of the specification.

XX Minimal promoter, tetracycline responsive expression vector; TREV;

XX transcriptional transactivation domain; TTD;

XX tetracycline repressor protein; TRP; tetracycline operator;

XX production; stable cell line; protein production;

XX tumour suppressor protein; treatment; cancer; ss.

XX Unidentified.

XX Key

XX CDS

XX Location/Qualifiers

XX 7..2457

XX /tag- a

XX WC9837185-A2.

XX 27-AUG-1998.

XX 19-FEB-1998; 98W0-US03092.

XX 20-FEB-1997; 97US-0038755.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Hu S, Loqthelis CJ, Xu B, Zhou Y;

XX WPI: 1998-480796/41.

XX P-PSDB; AAW71355.

XX New tetracycline responsive expression vectors - used for the

XX tightly controlled expression of genes, such as tumour suppressor

XX genes for treating cancers

XX Disclosure; Pages 153-157; 190pp; English.

XX The present sequence appears in the specification, which describes a

XX tetracycline responsive expression vector (TREV), which contains a

XX sequence encoding a fusion protein comprising a transcriptional

XX transactivation domain (TAD) operatively attached to a tetracycline

XX repressor protein (TRP), the first sequence operatively positioned

XX downstream of a promoter. The vector also contains a cloning site

XX operatively positioned downstream of a basal promoter comprising a

XX tetracycline operator. The TREVs can be used to produce stable cell

XX lines in which gene expression is tightly regulated by tetracycline.

XX they can be used for the production of proteins such as tumour

XX suppressor proteins which can be used for treating diseases characterised

XX by abnormal cellular proliferation, particularly cancers.

XX SQ

SQ sequence 3218 BP; 1080 A; 595 C; 561 G; 982 T; 0 other;

XX

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Query Match 99.88; Score 3107; DB 19; Length 4218;
 Best local Similarity 100.08; Pred. No. 0;
 Matches 3107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 487 TCTAAATGGACATCCACAGAGTGTAAAAATCTTCTAAACCATACGAGAAATTTATCTTAAA 546
DB 640 TCTAAATGGACATCCACAGAGTGTAAAAATCTTCTAAACCATACGAGAAATTTATCTTAAA 699
QY 547 AATAAAGATCTAGATGCAAGATTTATTTTGGATATATGATTAAGATCTCTCAGACATGATCT 606
DB 700 AATAAAGATCTAGATGCAAGATTTATTTTGGATATATGATTAAGATCTCTCAGACATGATCT 759
QY 607 AATAGATACATCTTCAACACAGACAGACATCCACAAAAAGTAACTTGAATGAGAGAGGTGAAT 666
DB 760 AATAGATACATCTTCAACACAGACAGACATCCACAAAAAGTAACTTGAATGAGAGAGGTGAAT 819
QY 767 GTAAATCTCTCCATACACATCCACAGATCTGATTAAGACATCTCCACAAATTAATGATG 726
DB 820 GTAAATCTCTCCATACACATCCACAGATCTGATTAAGACATCTCCACAAATTAATGATG 879
QY 927 ATTTTAAATCTAGATGATGATTAATCTTCAAAAAATCTGATTTGATTAATTAATTAATG 786
DB 880 ATTTTAAATCTAGATGATGATTAATCTTCAAAAAATCTGATTTGATTAATTAATTAATG 939
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DB 1040 ATACATGAAATCCCAAAAGATATACGAGAAAGATCTCAAGGATATAGGATACATCTTTAAA 999
QY 1047 GAGAAATCTCTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 906
DB 1100 GAGAAATCTCTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1059
QY 1107 CTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 966
DB 1160 CTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1119
QY 1167 TTAATCTTCAAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1026
DB 1220 TTAATCTTCAAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1179
QY 1227 GGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1086
DB 1280 GGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1239
QY 1287 TGTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1146
DB 1340 TGTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1299
QY 1347 TTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1206
DB 1400 TTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1359
QY 1407 AAACATTTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1266
DB 1460 AAACATTTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1419
QY 1467 GCTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1326
DB 1520 GCTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1479
QY 1527 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1386
DB 1580 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1539
QY 1587 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1446
DB 1640 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1599
QY 1647 GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1506
DB 1700 GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1659
QY 1707 TCACTGTTTTTAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1566
DB 1760 TCACTGTTTTTAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1719

QY 1567 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1526
DB 1720 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1779
QY 1627 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1686
DB 1780 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1839
QY 1687 ATGTATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1746
DB 1840 ATGTATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1899
QY 1747 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1806
DB 1900 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1959
QY 1807 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1866
DB 1960 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2019
QY 1867 ATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1926
DB 2020 ATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2079
QY 1927 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1986
DB 2080 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2139
QY 1987 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2046
DB 2140 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2199
QY 2047 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2106
DB 2200 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2259
QY 2107 ATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2166
DB 2260 ATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2319
QY 2167 CTCTCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2226
DB 2320 CTCTCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2379
QY 2227 AGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2286
DB 2380 AGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2439
QY 2287 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2346
DB 2440 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2499
QY 2347 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2406
DB 2500 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2559
QY 2407 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2466
DB 2560 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2619
QY 2467 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2526
DB 2620 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2679
QY 2527 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2586
DB 2680 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2739
QY 2587 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2646
DB 2740 TGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2799

[illegible][illegible]


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1b 1447 TCTGTTGTCCTTAATGCTGCTCCAGAAATAATCAGATGCGAGAGATATGTAATCT 1596
1b 1448 TATGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1446
1b 1449 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1656
1b 1450 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1506
1b 1451 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1716
1b 1452 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1566
1b 1453 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1776
1b 1454 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1626
1b 1455 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1836
1b 1456 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1686
1b 1457 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1846
1b 1458 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1746
1b 1459 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1956
1b 1460 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1806
1b 1461 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2016
1b 1462 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1866
1b 1463 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2076
1b 1464 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1926
1b 1465 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2136
1b 1466 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 1986
1b 1467 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2186
1b 1468 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2046
1b 1469 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2256
1b 1470 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2106
1b 1471 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2316
1b 1472 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2166
1b 1473 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2376
1b 1474 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2226
1b 1475 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2436
1b 1476 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2286
1b 1477 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2496
1b 1478 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2346
1b 1479 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2556
1b 1480 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2406
1b 1481 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2616
1b 1482 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2466
1b 1483 TCTGCTGTAAGATCTCTTAAGAGAAAAGCTTCATATGCTGTGTAATATCTACTCAAAAT 2676

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QY 2467 CTCTTCTGCGATATAAAAAAGCGACATGCAAAATGCTTCTGCGATATAAAAAAGCGACATGCAAA 2526
Db 2677 CTCTTCTGCGATATAAAAAAGCGACATGCAAAATGCTTCTGCGATATAAAAAAGCGACATGCAAA 2736
QY 2527 ATCTTACTGCTGCTTATTTATACAAATGCAAAATGCTTCTGCGATATAAAAAAGCGACATGCAAA 2586
Db 2737 ATCTTACTGCTGCTTATTTATACAAATGCAAAATGCTTCTGCGATATAAAAAAGCGACATGCAAA 2796
QY 2587 ASHGGAGAGATGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTG 2646
Db 2797 ASHGGAGAGATGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTG 2856
QY 2647 ATGGGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2706
Db 2857 ATGGGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2916
QY 2707 TAGCATATAGGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTG 2766
Db 2917 TAGCATATAGGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTG 2976
QY 2767 AATCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2826
Db 2977 AATCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 3036
QY 2827 CCATTCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2886
Db 3037 CCATTCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 3096
QY 2887 AAAAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2946
Db 3097 AAAAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 3156
QY 2947 GCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCT 3006
Db 3157 GCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCT 3216
QY 3007 TGATCATATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 3066
Db 3217 TGATCATATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 3276
QY 3067 TATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3126
Db 3277 TATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3326

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RESULT 6

AAV58442

ID AAV58442 Standard; DNA; 3392 bp.

XX AAV58442;

XX 02-DEC-1998 (first entry)

XX Modified retinoblastoma tumor suppressor gene.

XX Modified retinoblastoma tumor suppressor E1F protein tumor therapy;

XX cellular proliferation inhibitor; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 7..2641

XX /*tao- a

XX W09837091-A2.

XX 27-AUG-1998.

XX 19-FEB-1998; 98W0-US03041.

XX 20-FEB-1997; 97US-0038118.

XX


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14 256  AATAAATATCTCCAGGAGAGTGTAAATTTATATGAAATGTAATAAATATCTACT 2628
15 2287  CGAACACGAATCGAAAGTACAAAAAGCAATGATAGCATGGATACCTCAATCAAGCAAG 2346
16 2624  CGAACACGAATCGAAAGTACAAAAAGCAATGATAGCATGGATACCTCAATCAAGCAAG 2688
17 2447  AAAATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2406
18 2489  AAATGAGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2748
19 2457  CAATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2456
20 2744  CAATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2808
21 2167  CTTTCTGATATATAAATGTCATGCAATGTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2526
22 2809  CTTTCTGATATATAAATGTCATGCAATGTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2868
23 2727  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2586
24 2869  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2928
25 2187  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2646
26 2729  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2688
27 2447  AAAATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2706
28 2789  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3048
29 2767  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2766
30 3049  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3108
31 2767  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2826
32 3049  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3184
33 2827  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2886
34 3169  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3228
35 2887  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2946
36 3229  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3288
37 2947  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3006
38 3289  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3348
39 3007  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3066
40 3449  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3408
41 3067  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3113
42 3409  ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3455

RESULT 8
AAV68447
ID  AAV68447 standard. DNA. 3401 BP.
XX
XX  AAV68447:
XX
XX  02 DEC 1998 (first entry)
XX
XX  Modified retinoblastoma tumour suppressor gene.
XX
XX  Modified retinoblastoma tumour suppressor: RPS protein; cancer therapy.
XX
XX  Cellular proliferation inhibitor; ss.
XX
XX  Homo sapiens.

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XX
FH Key Location/Qualifiers
FT CDS 7..2700
FT /*tag= a
XX WC09837091-A2.
XX
XX 27-AUG-1998.
XX
XX 19-FEB-1998; 98WO-US01041.
XX
XX 20-FEB-1997; 97US-0038118.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX (LEXA ) UNIV TEXAS SYSTEM.
XX
XX Benedict WF, Hu S, Xu H, Zhou Y:
XX WPI: 1998-480/88/41.
XX P-PSDB: AAM69471.
XX
XX Retinoblastoma suppressor protein with N-terminal modification -
XX inhibiting cellular proliferation, particularly cancer
XX
XX Claim 32: Page 188-192; 24pp; English.
XX
XX this sequence encodes a modified retinoblastoma tumour suppressor
XX protein (RPS) of the invention. the proteins can be used for inhibiting
XX cellular proliferation, when coadministered with a p53 protein. the RPSs
XX can be used for treating diseases characterized by abnormal cellular
XX proliferation, particularly cancers. The RPSs have a broader spectrum of
XX activity than wild type RPSs.
XX
XX Sequence 3461 bp; 1141 A; 675 C; 627 G; 1018 T; 0 other;
XX
XX Query Match 99.8%, Score 3107, DB 19; Length 3461;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 ATCTCAAGACTGTTCAGAAATATGATGATGTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 66
XX 355 ATCTCAAGACTGTTCAGAAATATGATGATGTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 414
XX 67 ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 126
XX 415 ATATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 474
XX 127 GATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 186
XX 475 GATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 534
XX 187 ATGGAAGATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 246
XX 535 ATGGAAGATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 594
XX 247 AAATCTCAATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 406
XX 595 AAATCTCAATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 454
XX 307 GATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 466
XX 655 GATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 714
XX 367 GAAATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 426
XX 715 GAAATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 774
XX 427 GTGAAATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 486
XX 775 GTGAAATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 844
XX 487 TGTATGATATCTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 546
XX

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16 845 TTTAAAGAGTTCAGAGGCTGCAAAATCTTTCTAAAGCAAGCAAGAAATTTATCTTAAA 894
17 847 AATAAAT 606
18 849 AATAAAT 954
19 851 AATAAAT 666
20 853 AATAAAT 1014
21 855 AATAAAT 726
22 857 AATAAAT 1074
23 859 AATAAAT 786
24 861 AATAAAT 1134
25 863 AATAAAT 846
26 865 AATAAAT 1194
27 867 AATAAAT 906
28 869 AATAAAT 1254
29 871 AATAAAT 966
30 873 AATAAAT 1314
31 875 AATAAAT 1026
32 877 AATAAAT 1374
33 879 AATAAAT 1086
34 881 AATAAAT 1434
35 883 AATAAAT 1146
36 885 AATAAAT 1494
37 887 AATAAAT 1206
38 889 AATAAAT 1554
39 891 AATAAAT 1266
40 893 AATAAAT 1614
41 895 AATAAAT 1326
42 897 AATAAAT 1674
43 899 AATAAAT 1386
44 901 AATAAAT 1734
45 903 AATAAAT 1446
46 905 AATAAAT 1794
47 907 AATAAAT 1506
48 909 AATAAAT 1854
49 911 AATAAAT 1566
50 913 AATAAAT 1914
51 915 AATAAAT 1626
52 917 AATAAAT 1974

1627 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 1686
1629 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2044
1631 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 1746
1633 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2094
1635 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 1806
1637 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2154
1639 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 1866
1641 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2214
1643 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 1926
1645 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2274
1647 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 1986
1649 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2334
1651 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2046
1653 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2494
1655 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2106
1657 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2454
1659 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2166
1661 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2514
1663 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2226
1665 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2574
1667 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2286
1669 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2634
1671 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2346
1673 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2694
1675 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2406
1677 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2754
1679 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2466
1681 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2814
1683 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2526
1685 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2874
1687 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2586
1689 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2934
1691 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2646
1693 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2994
1695 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 2706
1697 CTGCACAAATCAGTATCAAACTCATGACAGACAGAGATTTTGGAGCAAAATATATGAGTGGT 3054

Additional constructs include a papilloma virus E7 protein, or other viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of the Rb and p16INK4a genes may also be used. The methods are useful for increasing the proliferative capacity of cells. The cells are subsequently of use in pharmaceutical and cosmetic preparations used to treat conditions related to (premature) ageing, e.g. macular degeneration and arteriosclerosis, the cells can also be used to replace tumour cells and arteries in vivo and for studies on biochemical and physiological aspects of growth and differentiation. Long lived (immortal) cells could also be of use in the production of normal or genetically engineered biotechnology products.

Sequence 4949 bp; 1534 A; 992 C; 880 G; 1523 T; 0 other;

[illegible]

result of ML and the data is sufficient to convey the chemical structure and/or properties of the agent. ML can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

XX
SQ Sequence 4839 BP: 1534 A: 902 C: 880 G: 1523 T: 0 other:

Query Match 99.8% Score 3107; DB 24; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 AIGCAAGATGTCGAAGAGTATGATGTTGTCACCTTCACGCAAAATTCGAAGG 66
|||||
67 AIGCAAGATGTCGAAGAGTATGATGTTGTCACCTTCACGCAAAATTCGAAGG 638
|||||
67 AATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 126
|||||
68 AATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 698
|||||

127 GATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186
|||||
699 GATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 758
|||||

187 AIGCAAGATGTCGAAGAGTATGATGTTGTCACCTTCACGCAAAATTCGAAGG 246
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259 AIGCAAGATGTCGAAGAGTATGATGTTGTCACCTTCACGCAAAATTCGAAGG 818
|||||

247 AATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 306
|||||

819 AATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 878
|||||

307 GATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
|||||

879 GATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938
|||||

467 GAAATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
|||||

939 GAAATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 998
|||||

427 GTCAAAATGCTTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
|||||

999 GTCAAAATGCTTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1058
|||||

487 GTCAAAATGCTTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
|||||

1059 GTCAAAATGCTTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1118
|||||

547 AATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 606
|||||

1119 AATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 1178
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607 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 666
|||||

1179 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 1238
|||||

667 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 726
|||||

1239 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 1298
|||||

727 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 786
|||||

1299 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 1358
|||||

787 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 846
|||||

1359 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 1418
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847 GATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
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1419 GATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1478
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907 CTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
|||||

1479 CTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1538
|||||

967 TTAAGATTCAGAAATTTTAAAGAAATTTGTAATGATGATGATGATGATGATGATG 1026
|||||

1539 TTAAGATTCAGAAATTTTAAAGAAATTTGTAATGATGATGATGATGATGATGATG 1598
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1027 GCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
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1599 GCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1658
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1779 AAACATTTAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1838
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1267 CCTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1326
|||||

1839 CCTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1898
|||||

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1899 TCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1958
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|||||

1959 TCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2018
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|||||

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|||||

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|||||

1627 GCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686
|||||

2199 GCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2258
|||||

1687 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 1746
|||||

2259 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 2318
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2319 TAAAGATTCAGAAATTTTAAAGAAATTTGTAATGATGATGATGATGATGATGATG 2378
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1807 GATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1866
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2379 GATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2438
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1867 ATATGAACTTATATATTTGAATATATGAAAGAGTATGATATGATATGAAATATC 1926
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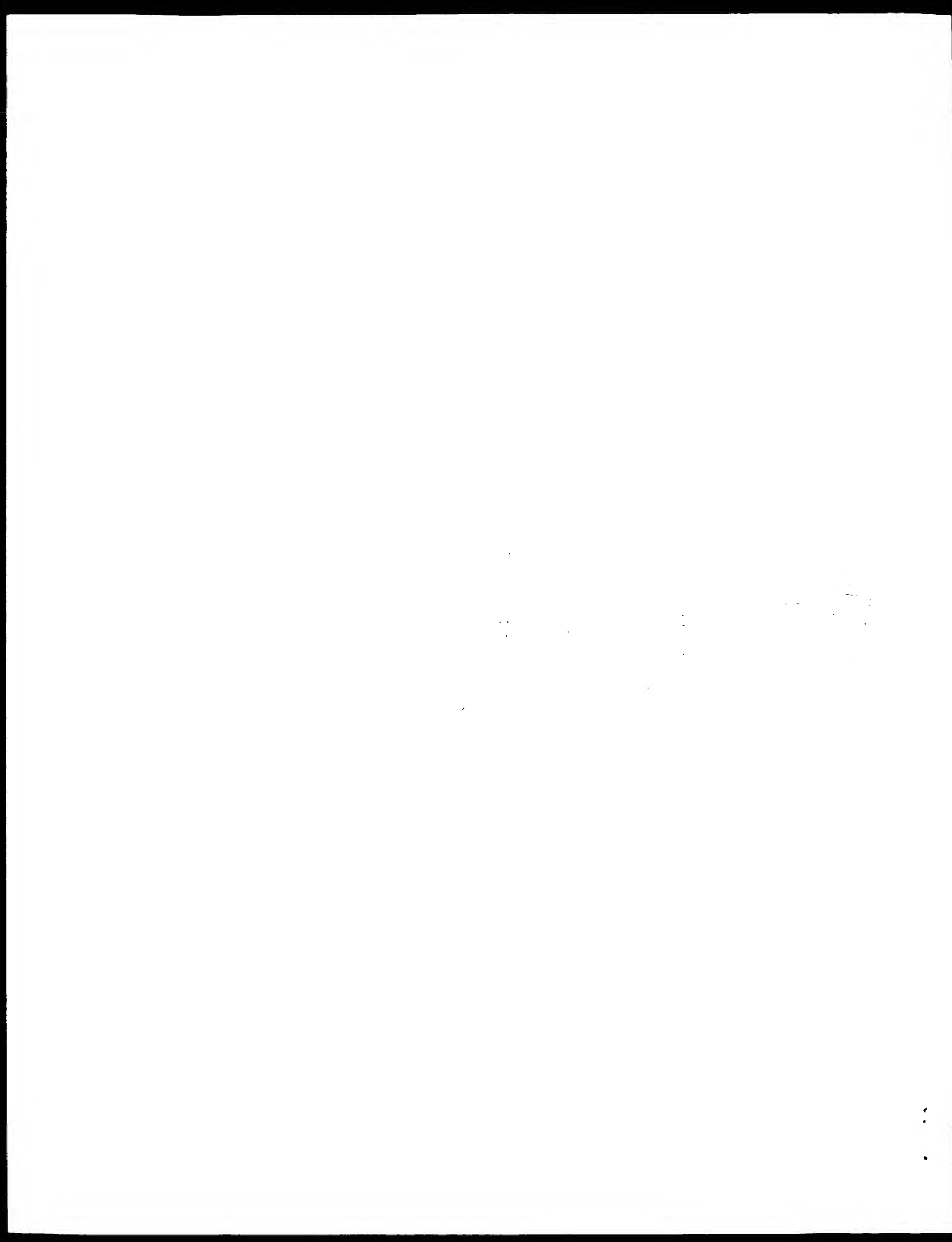
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1927 GATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1986
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2499 GATATGCTGCTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2558
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DB 2842 CACAGTGTACTATATAAATTTTGGAGTTCTGTGTTTATAGGGCAVATTTAAATATATCTAGCT 2901
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DB 2467 CTTTTGGGCAATAAAAAAGTGGACATACCAATTCGTTGGGTCATTCCTAAGCCACATGAA 2526
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DB 2902 CTTTTTGGGCAATAAAAAAGTGGACATACCAATTCGTTGGGTCATTCCTAAGCCACATGAA 2961
07
DB 2527 ATGTTAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 2586
07
DB 2962 AAGTTAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 3021
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DB 2587 AATGCTAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 2646
07
DB 3022 AATGCTAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 3081
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DB 2647 AAGGCTCTAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 2706
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DB 3082 AAGGCTCTAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 3141
07
DB 2707 TACATATAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 2766
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07
DB 2767 AATGCTCTAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 2826
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07
DB 2827 CCAATCTCTAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 2886
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DB 3262 CCAATCTCTAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 3321
07
DB 2887 AAAAAATCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 2946
07
DB 3322 AAAAAATCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 3381
07
DB 2947 CTTGCTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 3006
07
DB 3382 CTTGCTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 3441
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07
DB 3502 TATTTCTCTAGTCTATGTTTATTATATACAGATTTGAATCTTTGTGTAATGCTGGCATTTAAAA 3548

Search completed: January 16, 2003, 24:37:14
File time: 437.872 secs



Genature version 5.1.4
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M protein nucleic search, using frame_plus_p2n model

Run on: January 16, 2003, 23:41:08 : Search time 298.07 seconds
(without alignments)
7011.280 Million cell updates/sec

File: OS_09_026_459A_51

Perfect score: 4798
Sequences: 1 MPEPTPTFTATATAAAAP.....TMDKCKNNKSMCTSNKEEK 92R

Scoring table:

BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Scatched: 218549 seqs, 112599459 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4798	100.0	3554	19	AAV58452	Modified retinobla
2	4787	95.8	2994	14	AA041545	Retinoblastoma qen
3	4787	99.8	2994	19	AAV40004	Retinoblastoma pro
4	4787	99.8	2994	21	AAV40287	Wild type human re
5	4787	99.8	2995	20	AAV50450	Human p110 RB ret
6	4787	99.8	2995	22	AAH25765	Retinoblastoma tum
7	4787	99.8	2995	22	AAH04474	Retinoblastoma tum
8	4787	99.8	2995	23	ABL50904	Retinoblastoma tum
9	4787	99.8	3555	19	AAV58440	Modified retinobla
10	4787	99.8	3555	19	AAV54990	DNA sequence of th
11	4787	99.8	4839	21	AAV29491	Human retinoblasto
12	4787	99.8	4839	21	AAZ88444	Human androgen rec
13	4787	99.8	4839	24	ABL62873	Breast cancer rela
14	4783	99.7	2995	16	AAQ90959	Retinoblastoma tum
15	4778	99.6	2994	11	AAQ04713	Cancer suppressing
16	4778	99.6	2995	20	AAK00747	cDNA encoding a re
17	4772	99.5	2995	16	AAU86498	Human Rb10 cDNA
18	4739	98.8	4740	24	AAK86079	Human retinoblasto
19	4724.5	98.5	4597	15	AAK70516	Human retinoblasto
20	4721.5	98.4	4597	20	AAK04501	Human retinoblasto
21	4720.5	98.4	4597	9	AAH1369	Human retinoblasto
22	4599	95.9	3455	19	AAV58441	Modified retinobla
23	4597	95.8	4579	9	AAH1261	Probe for retinobl
24	4595.5	95.8	3461	19	AAV58447	Modified retinobla
25	4553.5	94.9	5056	10	AAV90489	cDNA of human ret
26	4489	93.6	3392	19	AAV58442	Modified retinobla
27	4444.5	92.6	3377	19	AAV58450	Modified retinobla
28	4437.5	92.5	3383	19	AAV58451	Modified retinobla
29	4398.5	91.7	3347	19	AAV58448	Modified retinobla
30	4357	90.8	3323	19	AAV58443	Modified retinobla
31	4323.5	90.1	3323	19	AAV58446	Modified retinobla
32	4263	88.8	3266	19	AAV58444	Modified retinobla
33	4204	87.6	4243	14	AAU72540	Retinoblastoma 'ak
34	4192	87.4	3218	19	AAV54991	DNA sequence of th
35	4068.5	84.8	3161	19	AAV58449	Modified retinobla
36	4017	83.7	3113	19	AAV58445	Modified retinobla
37	2153.5	44.9	18302	20	AAK04562	Human retinoblasto
38	2046.5	42.7	18177	10	AAV90490	DNA of human retin
39	837	17.4	4853	24	AAK84660	Human cDNA differe
40	816.5	16.9	3969	24	AAK84643	Human cDNA differe
41	809.5	16.9	4130	24	AAV54981	Human DNA sequence
42	756	15.8	2898	13	AAU2665	Nearly complete p1
43	754	15.7	3249	16	AAU82748	p142 retinoblastom
44	647.5	14.3	3292	23	AAU81194	cDNA encoding model
45	542.5	11.7	6745	23	AAU81194	cDNA encoding model

ALIGNMENTS

RESULT 1
AAV58452
1: AAV-2152 standard, cDNA, 554 bp.

XX AAV58452:

DI 92-DEC-1998 (first entry)

XX Modified retinoblastoma tumour suppressor gene.

XX Modified retinoblastoma tumour suppressor, Rb1 protein; cancer therapy;
cellular proliferation inhibitor; ss.

XX Homo sapiens.

XX Key location/Qualifiers

FT CDS 7..2793

FT /*tag= a


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1567 CTAAATTTAAAGAGCTTGGATTTTACAAAGTGGATGAGAACTTTATCAAAAGCAGAGGC 1626
QY 541 AsnLeuThrArgMetIleLysHisLeuGluArgCysGluHisArgGluMetCysSer 560
DB 1627 AACTTGAACAGAGAAATATATAAAATATTAGAACGATGTGAATATCGAATATGGAATCC 1686
QY 561 LeuAlaTyrLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 580
DB 1687 CTGGCAAGCTGTCACATTCACATTCATTAATGATCTATTAAACCAATCAAGACGACGACAA 1746
QY 581 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 600
DB 1747 GATCAATGATACAGCTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1806
QY 601 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysLysLysLysLys 620
DB 1807 ATTCAGCAGATATGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1866
QY 621 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 640
DB 1867 GGGGAAAAATGACGCAAAAGCAGAGACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1926
QY 641 ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeu 660
DB 1927 CATGTAATCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1986
QY 661 ArgGluAsnThrLeuCysThrArgLeuLeuSerGluHisProGluLeuGluHisIleIle 680
DB 1987 GGGTAAATATGCTTTGGTGAAGAGCTTCTGCTGAGCAAGCAAGCAAGCAAGCAAGCAAG 2046
QY 681 TrpThrLeuPheGluHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 700
DB 2047 TGGAGCTCTTTCACACACACGCGAGCAATGACATGACATGACATGACATGACATGACAT 2106
QY 701 AspIleIleLeuMetCysSerMetTyrGlyLysLysValLysAspIleAspLeuLys 720
DB 2107 GACCAATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2166
QY 721 PheGlyIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLys 740
DB 2167 TTTCAAAATATTAAACAGATACAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2226
QY 741 ArgValLeuIleLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 760
DB 2227 GGGGCTTTCATCAAAACAAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2286
QY 761 MetGlnAlaLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSer 780
DB 2287 ATGCAACACTGAAACAAATATTTGCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2346
QY 781 ProIleProHisIleProArgSerProLysPheProSerProLeuArgIlePro 800
DB 2347 CCAATATGCTGCAATGCTGCAATGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2406
QY 801 GlyGlyAsnIleLysIleSerProLeuLysSerProTyrLysIleSerGluCysLeuPro 820
DB 2407 GAGAGAAATATCAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2466
QY 821 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyLysSerPheGly 840
DB 2467 AATCAACAAATATGCTGCAATGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2526
QY 841 ThrSerGluLysPheGluLysIleAsnGlnMetValCysAsnSerAspArgValLeuLys 860
DB 2527 ATTTGCAAGATGCTGCAAAATAATAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2586
QY 861 ArgSerAlaGluLysAsnProLysProLeuLysLysLeuArgPheAspIleGlu 880
DB 2587 AATAGCTGCAAGAGCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2646
QY 881 GlySerAspGlnAlaAspLysSerLysHisLeuProGlyLysLeuSerLysPheGluLys 900

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DB 2647 GGATCAATATGAAGCAATGGAATTAACATATCTCTCAAGAGACTCTCAAAATTTATCAATCAAA 2706
QY 901 LeuAlaGluMetIleSerThrArgIleArgMetGluLysGlnLysMetIleAsnAspSerMet 920
DB 2707 CTGGCAAAAAGACATCTACTCGAACACAGAACTGAAAAGCAGAAAAGAAATATATGATG 2766
QY 921 AspThrSerAsnLysGlnGluLys 928
DB 2767 GATACCTCAACCAAGCAAGAGAGAAA 2790
RESULT 2
AAQ41545
ID AAQ41545 standard: DNA: 2994 bp.
XX AAQ41545:
AC
DI 24-AUG-1993 (first entry)
XX Retinoblastoma gene.
DE RB gene product: p56RB portion; cell cycle progression control;
KW combination; therapeutic methods; arrest; tumorigenesis;
KW regulation; physiological processes; blood cell production;
KW gamete production; ss.
XX Homo sapiens SR 40 cell line.
XX Key Location/Qualifiers
FH CDS 139..2945
FT /*aa= "a"
FT /note= "RB protein"
XX W09408267 A.
PN 29-AUG-1993.
DB 16-OCT-1992: 9280-0508918.
XX 17-OCT-1991: 9105-0778510.
XX (REGC ) UNIV CALIFORNIA.
XX Goodrich DW, Lee EYHP, Lee WH, Wang NP:
DB W01: 1993-152462/18.
DB P-PSDB: AAR36534.
XX Method of controlling cell cycle progression - uses purified
retinoblastoma protein or fragment, for use in combination with
therapeutic methods to arrest tumorigenesis
XX Disclosure: Fig 9: 68pp; English.
XX The sequence is that of the retinoblastoma gene which encodes the
retinoblastoma (RB) protein which may be used as part of a method of
controlling cell cycle progression which may be used in combination
with therapeutic methods to arrest tumorigenesis in organisms. The
cell cycle can be reversibly arrested in a convenient and safe
manner. The protein is used in a composition which is relatively inexpensive
and readily obtainable, and shows little or no toxic effects on
healthy cells. It is also compatible with other methods and devices
for regulating certain physiological processes of the body, such as
blood cell production and gamete production. Fragments of the protein are
soluble in low concentrations of glycerol thus enhancing their value in
pharmaceutical applications.
XX Sequence 2994 bp; 974 A; 618 C; 594 G; 808 T; 0 other;
Alignment Scores:
Pred. No.: 0 Length: 2994
Score: 4787.00 Matches: 926
Percent Similarity: 99.89% Gaps/align: 1
Best Local Similarity: 99.78% Mismatches: 1

```



```

QY 861 AqSsrAlaGluGlySerAspProProLysProLeuLysLysLeuArqPheAspIleGlu 880
DB 2719 ACAAATGCTCAAGCAAGCAATGCTCTTAAACCACTCAAAAAACCTACGCTTCATATTCGA 2778
QY 881 GlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPheGluGlnLys 900
DB 2779 GATCAATAGATGAAGAGATGGAAGTAAATATCTCTCAGAGAGATGCAAAATTTTAAAGAA 2838
QY 901 LeuAlaLeuMetThrSerThrArqThrArqMetGluLysGlnLysMetAspSerMet 920
DB 2839 CTGGTAAACCAACATCTTACCTAACACGAACTCAAAAGCAGAAAAACAAATCAATCAATC 2898
QY 921 AspThrSerAsnLysGlnLys 928
DB 2899 CATACTTAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2922
RESULTS 4
AAZ40287
ID AAZ40287 standard: cDNA: 2994 BP.
XX AAZ40287:
XX
XX 24 FEB 2000 (first entry)
XX
DE Wild type human retinoblastoma gene.
XX
KW RB gene; human; retinoblastoma gene; mutation detection; immunoscreening;
KW retinoblastoma diagnosis; hereditary retinoblastoma; secondary cancer;
KW osteosarcoma; fibrosarcoma; glioblastoma; breast cancer;
KW tumourigenesis suppressor; ss
XX Homo sapiens.
XX
XX OS9998134 A.
XX
XX 07 DEC 1999.
XX
XX 07 JUN 1995: 950S 0482627.
XX
XX 15 OCT 1987: 870S 0108748.
XX
XX 28 SEP 1992: 92BS 0951947.
XX
XX (BEOC) ONIV CALLIPORNIA.
XX
XX Lee EPP, Lee W.
XX
XX WPI: 2000 052540/04.
XX
XX P RSDB: AA55060.
XX
XX Detecting retinoblastoma gene-cancer in mammals -
XX
XX Example 6: Fig 7: 34pp: English.
XX
XX This sequence represents the wild type human retinoblastoma gene.
XX The invention relates to a method of detecting a mutated retinoblastoma
XX (mrb) nucleic acid in mammals comprising hybridizing an isolated
XX full length, wild type RB (wRB) cDNA probe to a cell sample and
XX detecting a mutated RB nucleic acid. The method is useful as a diagnostic
XX tool for diagnosing retinoblastoma. RB cDNA or genomic DNA are preferably
XX used as probes to determine the detect region of the mrb gene through
XX genomic DNA blotting analysis or using the method of restriction fragment
XX length polymorphism analysis to determine the diagnosed allele. Cloned RB
XX cDNA can be used to generate specific anti-RB protein (anti-pRB110)
XX antibodies which are useful for immunoscreening of tissue biopsy. The
XX diagnostic method is particularly intended for use in screening
XX families with a history of hereditary retinoblastoma and for screening
XX their children. It may also be used in prophylactic and postnatal
XX screening and for the prediction of the development of secondary
XX cancer, such as, osteosarcoma, fibrosarcoma, glioblastoma, breast
XX cancer whether or not connected with retinoblastoma. The method is also
XX used in the suppression of tumourigenesis where the absent RB protein
XX pRB110 will be provided through the molecular induction and gene
XX transplanted of the RB cDNA to the individual in need of pRB110.

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XX
SQ Sequence 2994 BP: 974 A: 618 C: 594 G: 808 T: 0 other:
Alignment Scores:
Pred. No.: 0 Length: 2994
Score: 4787.00 Matches: 926
Percent Similarity: 99.89% Conservativ: 1
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.77% Indels: 0
DB: 21 Gaps: 0
US-09-026-459A 51 (1-928) x AA240287 (1-2994)
QY 1 MetProGlySerThrProArqLysThrAlaAlaThrAlaAlaAlaAlaAlaAlaGluPro 20
DB 139 AUGCGGCGCAAAAGCCGCCCAAAACCGGCGCCACGCGGCGCGCGCGCGCGCGCGCGCG 198
QY 21 ProAlaProProProProProProProProProGluAspProGluAspSerGlyProGlu 40
DB 139 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 258
QY 41 AspLeuProLeuValArqLeuGluPheGluThrAlaGluThrAlaGluThrAlaGluThr 60
DB 259 GACCTGCTCTCTCGTCAGGCTTGAGCTTTGAGAACAGAACAGAACAGAACAGAACAGAAC 418
QY 61 CysGlnLysLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 80
DB 319 TCTCAGAAATTAAGATACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 478
QY 81 ValSerSerValAspGlyValLeuGlyLysLysLysLysLysLysLysLysLysLysLys 100
DB 379 GTTTCATCTGTGATGAGTATGTGGAGGTATATATCAAAAGAAAGAAAGAAAGAAAGTCT 438
QY 101 IleCysLysPhePheAlaAlaValAspLeuGlyAspMetSerPheThrPheThrGluLeu 120
DB 439 ATCTGATCTTTATTTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 498
QY 121 GlnLysAsnIleGluIleSerValHisLysPhePheAspLeuLeuLysGluIleAspThr 140
DB 499 CAGAAAAACATAGAAATCAGTGTGCAATAATCTTAACTTAACTTAACTTAACTTAACTT 558
QY 141 SerThrLysValAspAspAlaMetSerArqLeuLeuLysLysLysLysLysLysLysLys 160
DB 559 AGTACCAAGATTTGATATGCTATGTCAGATGCTGAGAGATGATGATGATGATGATGATG 618
QY 161 LeuPheSerLysLeuGluArqThrCysGluLeuIleIleIleIleIleIleIleIleIle 180
DB 619 CTCTTCAGCAAAATTTGAAAGGACATGTGAACTTATATATATATATATATATATATATAT 678
QY 181 IleSerThrGluIleAsnSerAlaLeuValLeuLysValSerThrPheThrPheLeuLeu 200
DB 679 ATATCTACTGAAATTAATTTCCCAATGCTGCTTAAAGATTTCTTGGATCACTATTTATTA 738
QY 201 AlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheThrIleLeuMetLe 220
DB 739 GCTAAAGGGAGATTTACAAATGAGAGATGATGCTGTGATTTTCATTTTAAATATGCTA 798
QY 221 CysValIleCysPhePheLysLysSerThrProMetIleLeuLysLysLysLysLysLys 240
DB 799 TGTGTCTTGTACTATTTTATTAATCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 858
QY 241 ThrAlaValLysPheGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 260
DB 859 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 918
QY 261 AlaArqIleAlaLysGlnLeuLeuGluAsnAspThrArqIleIleGluValLeuCysLysGlu 280
DB 919 GATGATAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTA 978
QY 281 HisGluCysAsnIleAspGluValLysLysValLysPheLysAsnPheIleProPheMet 300
DB 979 CATGAATGTAATATAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1038

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us-09-026-459a-51.rng

Tue Jan 21 10:04:49 2003

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601 AsnSerLeuGluValThrSerAsnGlyGlyProGluValGlnAsnLeuSerLysArg 320
|||||
1009 AATTCCTTGGACCTTGTACATCTAATGAGCTTACAGAGCTTGAAGATCTTCTTAACGGA 1008
|||||
421 TTTGAGGluGluLeuTyrLeuLysAsnLysAspLeuAspAlaLeuPheLeuAspHisAsp 340
|||||
1009 ACCAACAATTAATCTTAAAAATAAAGATCTAGATGCAACATTAATTTTGGATCATCAT 1158
|||||
441 LysThrLeuGluThrAspSerIleAspSerPheGluThrGlnArgThrProArgLysSer 360
|||||
1159 AAAACCTCTTCAGACTGATCTATAGACAGTTTGAACACACAGAACACCACGAAAAAGCT 1218
|||||
461 AsnLeuAspGluGluValAsnValIleProProHisThrProValArgThrValMetAsn 380
|||||
1219 AACCTTCATGAAGAGGTGAATGTATTCCTGCACACATCTCAATTAAGACATGATTAAG 1278
|||||
681 ThrIleGlnGlnLeuMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 400
|||||
1279 ACATACCAACAAATTAAGATGATTTTAAATTCAGCAAGTATCAACCTTCAGAAATCTG 1338
|||||
401 IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgValLys 420
|||||
1439 ATTTCCTATTTTAAACAACCTGCACAGTGAATCCCAAGAGAAAGATACTGMAAGAGTGA 1498
|||||
421 AspIleGlyTyrIlePheGlyGluGlyPheAlaLysAlaValGlyGlnGlyCysValGln 440
|||||
1499 GATATAGATATCATCTTTAAGAGAAATTTGCTTAAGCTGTGAGACAGATGTGTCGAA 1458
|||||
441 IleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMet 460
|||||
1459 ATTGGAATCACACGACATACAACTTCGAGTTCGTTGTATTACCGAGTAATCGAATCCATG 1518
|||||
461 LeuLysSerGluGluGluArgLeuSerIleGluAsnPheSerLysLeuLeuAsnAspAsn 480
|||||
1519 CTTAATACAGAGAGAGAGATTAATCAATTCAAAATTTAGCAACCTTCGAAATACAAAC 1578
|||||
481 IlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 500
|||||
1579 ATTTCCTATATGCTTTATTTGAGAGTGGATTTTCAGGTTGTAATGGACAAATATAGAT 1638
|||||
501 SerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPheProThrIleLeuAsnVal 520
|||||
1639 AGTACATCTCAGATCTGATCTGCAACAGATTTGCTTTCCCATGCGATCTCAATGTCG 1698
|||||
521 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly 540
|||||
1699 GTTAATTTAAAGGCTTTGATTTTACAAAGTATGATGAGAACTTTTATCAAAAGAGAGG 1758
|||||
541 AsnLeuThrArgGluMetIleLysHisLeuGluArgGlyGluHisArgIleMetGluSer 560
|||||
1759 AACCTGACAGAGAAATGATTAATTTAATGATGAGAAATGATGATGATGATGATGATG 1818
|||||
561 LeuAlaThrLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 580
|||||
1819 CTGCAAGCTCTCAGATCTGATCTGATGATGATGATGATGATGATGATGATGATGATG 1878
|||||
581 GlyPheThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnHis 600
|||||
1879 GGAGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1938
|||||
601 ThrAlaAlaAspMetTyrLeuSerProValIleArgSerProLysLysGlySerThrThr 620
|||||
1939 ACTGACAGAGATATGATCTCTCTGCTGTAAGATCTCAAAAGAAAAAGTCAACATAGC 1998
|||||
621 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 640
|||||
1999 CGTGTAAAATCTCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2058
|||||
641 ProLeuLysSerThrSerLeuSerPhePheTyrLysLysValTyrArgLeuAlaTyrLeu 660
|||||
2059 CATTGAATATCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2118
|||||
661 ArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIle 680

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6119 CCGCTTAATAATACATTTGCTGAACCCCTTCTGTCGACCAACAGAAATTAGAACATATCA 2178
|||||
681 TrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGlnLeuMetArgAspArgHisLeu 700
|||||
2179 TGGACCCCTTTCCAGCAACACCCGACAGAAAGATATCAAACTCATGAGACACATCATTT 2238
|||||
701 AspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnHisCaspLeuLys 720
|||||
2239 GACCAAAATATGATGTGTTCATGATATGGCATATGCAAGATGAGAGATATAGAGCTTAAA 2298
|||||
721 PheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGlnIleThrPheLys 740
|||||
2299 TTTCAAAATCATTTGACACAGCATACAGGATCTTCCATCTGCTTCAGAGACATTCAAA 2358
|||||
741 ArgValLeuIleLysHisIleGluTyrAspSerIleIleValPheTyrAsnSerValPhe 760
|||||
2459 CGTGTCTTTCATCAACAAAGAGAGATATGATCTATCTATATAGTATCTTATPAACCTG 2418
|||||
761 MetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProThrThrLeuSer 780
|||||
2419 ATGACAGAGATGAAAGCAATATTTTTCATCTATCTATCTATCTATCTATCTATCTAT 2478
|||||
781 ProIleProHisIlePheArgSerThrTyrLysPheProSerSerThrLeuArgIlePro 800
|||||
2479 CCAATATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 2538
|||||
801 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeuPro 820
|||||
2539 GCAAGCAACATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 2598
|||||
821 ThrProThrLysMetThrProArgSerArgIleLeuValIleGlyGluSerPheGly 840
|||||
2599 ATCAACAAATGATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 2658
|||||
841 ThrSerGluLysPheGlnLysIleAsnGlnMetValCysSerAspArgValLeuLys 860
|||||
2659 ACTTCTGACAACTTCCAGAAATATAATCATCATGATGATGATGATGATGATGATGATG 2718
|||||
861 ArgSerAlaGluGlySerAsnProLysProLysProLysLeuLysLeuArgPheAspIleGln 880
|||||
2719 AGAAGTCTGAGAAATCAAGCAACCTCTTAAACCACTCAAAACCACTCAAAACCACTCA 2778
|||||
881 GlySerAspGluAlaAspGlySerLysHisLeuProGlyLysLeuSerPheGlnGlnLys 900
|||||
2779 GGATCATGATGAGCAGATGGAAGTAAACATTTTCAGAGAGAGTCCAAATTTTCAGCAG 2838
|||||
901 LeuAlaGluMetThrSerThrArgMetGlnLysGlnLysMetAsnAspSerMet 920
|||||
2839 CTGGCAGAAATGATCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 2898
|||||
921 AspThrSerAsnLysGluGluLys 928
|||||
2899 CATACCTCAACAAAGCAACAGAAA 2922
|||||
RESULT 5
AAK90350
ID AAK90350 standard; cDNA; 2995 bp.
AC
XX AAK90350.
XX
XX 27-Sep-1999 (first entry)
XX Human p110-KB retinoblastoma tumour suppressor encoding cDNA.
XX Human p110-KB; retinoblastoma; tumour suppressor; gene therapy;
XX adenoviral protein IX; recombinant adenovirus expression vector;
XX cell cycle; p53; mitosis; cell death; apoptosis; thymidine kinase;
XX cancer; ss.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
PH

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QY 481 IlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 500
 DB 1175 AIIIIICAIAGICIIIIATIGGGGIGGGGICITIGAGGCTGIAATGGCCACATATACAGA 1638
 QY 501 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProThrIleLeuAsnVal 520
 DB 1649 AGIACATCTCAGATCTTGATTGGAACAGATTTCCTTTCCATGGATTCTGATATG 1698
 QY 541 LeuAsnLeuLysAlaPheAspPheTyrTysValIleCysSerPheIleLysAlaGluGly 540
 DB 1699 TIAAHTTAAAGSCCTTGATTTTAAAGAGTATGGAAGCTTTTATCAAGACAGAAAGC 1758
 QY 561 AsnLeuThrArgGluMetIleLysLysLeuGluArgCysGluHisArgIleMetGluSer 560
 DB 1759 AACITGAAACAGAGAAAGATAAAACATTTAGAACGATGTCACATGCAATCATGGAAATCC 1818
 QY 581 LeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 580
 DB 1819 GTTGATAGGTCTCAGATTCACCTTTATTTGATCTTATTATTAACAAATCAAGGACCGAGAA 1878
 QY 601 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnHis 600
 DB 1879 AGACAAATGATACCTTGAAATTCGTGPGCKCTTAACTTCCTCCAGAAATATATCAC 1938
 QY 621 ThrAlaAlaAspMetTyrLeuSerPheValAspSerPheLysLysLysSerThrThr 620
 DB 1939 AATGACAGCAATGATCTTCCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1998
 QY 641 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 640
 DB 1999 GATGTAATTTATATGTAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 2058
 QY 661 ProLeuLysSerThrSerLeuSerPheThrLysLysValTyrArgGluAlaTyrLeu 660
 DB 2059 GCATGAAATCTAGCTCTTTTCTTTTATATATATATATATATATATATATATATATAT 2118
 QY 681 ArgLeuAsnThrLeuGlySerAlaArgLeuLeuSerGlnHisProGlnLeuGlnHisIle 680
 DB 2119 GGGTAAAT 2178
 QY 701 TrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 700
 DB 2179 TAT 2238
 QY 721 AspGlnIleMetMetCysSerMetMetCysTyrIleCysLysValLysAsnIleCysPheLys 720
 DB 2239 GATCAAT 2298
 QY 741 PheLysIleIleValThrAlaThrLysAspLeuProHisAlaValGlnSerGluThrPheLys 740
 DB 2299 TCAAAAT 2358
 QY 761 ArgValLeuLysGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPhe 760
 DB 2359 GGTGTTTGTGACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2418
 QY 781 MetGlnArgLeuLysThrAsnIleLeuGlnTyrTyrAlaSerThrArgProThrLeuSer 780
 DB 2419 ATGATAGAGTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2478
 QY 801 ProIleProHisIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 800
 DB 2479 GCAATACCTTACATCTTCAAGGCTTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 2538
 QY 821 GlyLysAsnIleTyrIleSerProLeuLysSerProTyrLysLysSerProTyrLys 820
 DB 2539 GATAGAGAT 2598
 QY 841 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGluGluSerPheGly 840
 DB 2599 AATCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2658

QY 841 ThrSerGlnLysPheGlnLysIleAsnGlnMetValLysAsnSerAspArgValLeuLys 860
 DB 2659 ACITCTCAGAAAGTTCAGAGAAATAAATCAGATGGTAATGACACCCAGCCGTCCTCAAA 2718
 QY 861 ArgSerAlaGluCysSerAsnProProLysProLeuLysLysLeuArgPheAspIleGln 880
 DB 2719 AGAAGIGCTGAG 2778
 QY 901 CysSerAspCysAlaAspCysLysSerHisLeuPheCysCysSerLysPheGlnGlnLys 900
 DB 2779 GGATTCATGACAG 2838
 QY 921 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAspAspSerMet 920
 DB 2839 CTGGCAGAAATGACTTCTACTCGACACAGATCCAAACAGAGAGAGAGAGAGAGAGAG 2898
 QY 921 AspThrSerAsnLysGluGluLys 928
 DB 2899 GATACCTCAACCAAG 2922
 RESULT 6
 AAH25755
 ID AAH25755 standard; DNA; 2995 bp.
 AC AAH25755;
 DT 14-AUG-2001 (first entry)
 XX
 DE Retinoblastoma tumour suppressor gene.
 XX
 KW Retinoblastoma; tumour suppressor protein; pRb; p53; cancer;
 KW adenoviral vector; gene therapy; thymidine kinase; ds.
 XX
 QS Unidentified.
 XX
 FN US2001096629-A1.
 XX
 FD 05-JUL-2001.
 XX
 PP 24 NOV 1999; 99US-0449113.
 XX
 PP 25-OCT-1994; 94US-0328673.
 PP 25-OCT-1994; 93US-0142669.
 PP 14-MAY-1994; 94US-0245006
 XX
 (GREG/) GREGORY R J.
 PA (WILL/) WILLS K N.
 PA (MANE/) MANEVAL D C.
 XX
 FT Gregory RJ, Wills KN, Maneval DC;
 FT WFL, 2001:39270/42.
 DR P-PSDB; AAH98945.
 XX
 PT Recombinant adenovirus expression vector comprising a partial or total
 PT deletion of a protein IX DNA and a gene encoding a foreign protein e.g.
 PT suicide protein, useful for inhibiting or reducing the proliferation of
 PT a tumour e.g. brain tumour -
 XX
 PS Disclosure; Fig 3; 39pp; English.
 XX
 CC The present invention describes an adenoviral expression vector
 CC comprising a deletion in the protein IX gene and a gene encoding a
 CC foreign protein. This vector can be used in gene therapy, particularly to
 CC introduce tumour suppressor genes into cancerous cells. Genes which may
 CC be used include p53, thymidine kinase and retinoblastoma tumour
 CC suppressor gene (Rb). The present sequence is the retinoblastoma tumour
 CC suppressor gene.
 XX
 SQ Sequence 2945 bp; 975 A; 618 C; 593 G; 809 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 2995

QY 461 LeuYssSerGluGluAlaLeuSerTleGluAsnPheserTysLeuAsnAspAsn 480
 1387 CTIAAAATCAGAAAGAAACGATTAAGCAATCAAAATTTAGCAAACTTCGAAATGACAAAC 1446
 QY 481 TlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 500
 1447 ATTTTCATATAGTCTTATTTGGGTGGGGCTCTGAGGGTGTAAAGGACATATAGACAA 1506
 QY 501 SerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPheProThrPleLeuAsnVal 520
 1507 ACTATATCTAGAAATCTGATCTTCAACACATTTCTCTCTTCCATGATCTCGAATGTC 1566
 QY 521 LeuAsnLeuYsAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly 540
 1567 CTAAATTTAAAGGCTTTGATTTTACAAAGTCAAGCAAGCTTTTATCAAAAGCACAAGGC 1626
 QY 541 AsnLeuThrAlaGluMetIleLysHisLeuArgCysGluHisArgIleMetGluSer 560
 1627 AACTGACAAATATATATAAAATTTTATAGACGATGTCGAACTATGAAATCAGGATGTC 1686
 QY 561 LeuAlaThrLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 580
 1687 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1746
 QY 581 GlyProThrAspHisLeuHisSerAlaCysProLeuAsnLeuProLeuGluAsnHis 600
 1747 GATCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1806
 QY 601 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysGlySerThrThr 620
 1807 ACTGATGATATATATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1866
 QY 621 ArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAlaPheGluThrGlnLys 640
 1867 GAT 1926
 QY 641 ProLeuLysSerThrSerLeuSerLeuPheTyrLysValTyrArgLeuAlaTyrLeu 660
 1927 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1986
 QY 661 ArgLeuAsnThrLeuPysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIle 680
 1987 GAT 2046
 QY 681 ThrThrLeuPheGluHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 700
 2047 GAT 2106
 QY 701 AspGluIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 720
 2107 GAT 2166
 QY 721 PheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGluGluThrPheLys 740
 2167 TTTAAATCATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2226
 QY 741 ArgValLeuIleLysGluGluThrTyrAspSerIleLeuValPheLysAsnSerValPhe 760
 2227 GAT 2286
 QY 761 MetGluArgLeuLysThrAsnIleLeuGluThrAlaSerThrArgProProThrLeuSer 780
 2287 ATGAT 2346
 QY 781 ProLeuProHisIleProArgSerProLysPheProSerSerProLeuArgIlePro 800
 2347 GAT 2406
 QY 801 GlyGlyAsnIleThrSerProArgLysSerProTyrLysSerGlyLeuPro 820
 2407 GAT 2466
 QY 821 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyLysProPheThr 840

DB 2467 ATACCAATCAAAATGATCAAAATCAAAATTTAGTATCAATGATCAAAATTTAGTAT 2526
 QY 841 ThrSerGluLysPheGluLysIleAsnGluMetValCysAsnSerAspArgValLeuLys 860
 2527 ACTTCTGAGAGATTCCAGAAAAATTAATCAAGATGATGATGATGATGATGATGATGATGAT 2586
 QY 861 ArgSerAlaGluGlySerAsnProProLysProLeuLysLysLeuAlaGluAspIleGlu 880
 2587 AGAAGTGTCAAGGAGCAACCCGCTTAACCAACCAAAAAACATCAATCAATCAATCAATCA 2646
 QY 881 GlySerAspGluAlaAspGlySerLysHisLeuProGlyValSerLysPheAsnIleLys 900
 2647 GAT 2706
 QY 901 LeuAlaGluMetThrSerThrArgThrArgMetGluLysLysMetAsnAspSerMet 920
 2707 CTGCAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2766
 QY 921 AspThrSerAsnLysGluGluLys 928
 2767 CATACCTCAACCAAGGAGAGAGAA 2790
 RESULT 10
 AAV54990
 ID AAV54990 standard; DNA: 4555 BP.
 XX
 AC AAV54990;
 XX
 DT 26-NOV-1998 (first entry)
 XX
 DE DNA sequence of the specification.
 KW Minimal promoter; tetracycline responsive expression vector; TREV;
 KW transcriptional transactivation domain; tetracycline repressor protein; TRP; tetracycline operator;
 KW production; stable cell line; protein production;
 KW tumour suppressor protein; treatment; cancer; SS.
 XX Unidentified.
 OS
 FH
 ET CDS
 ET 7..2794
 ET /*aaq- a
 XX W09837185-A2.
 XX 27-AUG-1998.
 XX 19-FEB-1998; 98WO-US03092.
 XX 20-FEB-1997; 97US-0038755.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PL Hu S, Logothetis CJ, Xu H, Zhou Y;
 DR WPI: 1998-480796/4).
 DR P-SDH; AAW71354.
 XX New tetracycline responsive expression vectors used for the
 PT tightly controlled expression of genes, such as tumour suppressor
 PT genes for treating cancers
 XX Disclosure; Pages 145-150; 190pp; English.
 PS The present sequence appears in the specification, which describes a
 CC tetracycline responsive expression vector (TREV), which contains a
 CC sequence encoding a fusion protein comprising a transcriptional
 CC transactivation domain (TAD) operatively attached to a tetracycline
 CC repressor protein (TRP), the first sequence operatively positioned
 CC downstream of a promoter. The vector also contains a cloning site
 CC operatively positioned downstream of a basal promoter comprising a

421 CysValLeuAspTyrPheTleuLysSerProPheMetLeuLysGluProTyrLys 240
 148 IGTHGCTGACATATTTTATTAAGCTCAGCTGCAATGCTCAAAACATATATA 857
 441 ThrAlaValIleProIleAsnLysPheArgThrPheArgThrPheArgThr 260
 458 ACAGCTGATATAGCAATATATGCTTACCTTCAGCAACACCCAGCGAGTCA 917
 461 AlaAlaIleAlaLysGluLeuLysAspThrArgIleIleGluValLeuLysGlu 280
 478 GCAAGATACCAAAACATCAAAATGATACCAAAATATTAAGTTCTGTGAAGA 977
 481 HisGluLysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIleProPheMet 300
 478 CATCAATGATATATAGATGAGTGAAGAAATGTTATTTTCAAAATTTTATACCTTTATG 1037
 491 AsnSerLeuGluLeuValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArg 320
 148 AATTCCTGTCAGCTTGTAAACATCAAAAGACTTCCAGAGCTTCAAAATCTTTCTAAAGCA 1097
 421 TyrIleLeuIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAsp 340
 1098 TACCAAAATTTATCTTAAATAAAGATCTAGATGCAAGATTAATTTTGGATCATGAT 1157
 441 LysThrLeuGluThrAspSerIleAspSerPheGluThrGluArgThrProArgLysSer 360
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 461 AsnLeuAsnGluLeuValAsnValIleProPheIleThrProValArgThrValMetAsn 380
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 148 ATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1637
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 421 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly 540
 148 CITAAATCAAGAGAGATTTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1757
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 AAQ90059

Genature version 5.1.1.4
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M nucleic acid search, using sw model

Run on: January 16, 2003, 15:20:17 : Search time 4.44.554 Seconds
(without alignments)
17531.794 Million cell updates/sec

Filter: OS 09 026 459A 48
Perfect score: 4383
Sequence: 1 GGGGATGGGCGGAAAC.....AAATGACGATATGATAGT 3363

Scoring table: IDENTIFY NUC
Gapop 10.0, Gapext 1.0

Searches: 238249 seqs, 112595159 residues
Total number of hits satisfying chosen parameters: 4470478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post processing: Minimum Match 0%
Maximum Match 100%
Excluding first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	4383	100.0	3363	19	AAV58451
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5	4194.6	94.4	4849	21	AAZ88644
6	4194.6	94.4	4849	24	AB62873
7	4192.4	94.4	3554	19	AAV58450
8	4169	93.7	3477	19	AAV58450
9	4165	93.6	4597	15	AAQ70546

10	4165	93.6	4597	20	AAQ4501
11	4163.4	93.5	4597	9	AAAR1469
12	4160.4	93.4	4740	24	ABK86079
13	4119	92.2	4579	9	AAAR1261
14	4088.6	91.3	3455	19	AAV58441
15	4024.6	89.4	3452	19	AAV58442
16	2996.4	88.6	3461	19	AAV58447
17	2956.6	87.4	3423	19	AAV58443
18	2911.4	86.1	3447	19	AAV58448
19	2898.6	85.7	3264	19	AAV58444
20	2867.6	84.8	3323	19	AAV58446
21	2853.6	84.4	4218	19	AAV54991
22	2853	84.3	3233	15	AAZ272690
23	2757.4	81.5	3161	19	AAV58449
24	2748.6	81.2	3113	19	AAV58445
25	2662.6	78.7	5056	10	AAAG6489
26	2502.6	74.0	2994	19	AAV40004
27	2501	73.9	2994	14	AAZ41445
28	2501	73.9	2994	21	AAZ45287
29	2499.6	73.9	2995	20	AAZ90450
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31	2499.6	73.9	2995	22	AAH04474
32	2499.6	73.9	2995	23	AB650904
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35	2496.4	73.8	2995	20	AAQ03737
36	2493.2	73.7	2995	16	AAQ86398
37	835	24.7	18303	20	AAQ04502
38	831.8	24.6	18177	10	AAAG0490
39	220.8	6.5	1698	18	AAZ62390
40	220.8	6.5	1852	18	AAZ62391
41	220.8	6.5	2634	18	AAZ62354
42	220.8	6.5	3134	18	AAZ62353
43	220.8	6.5	3023	18	AAZ62356
44	218.8	6.5	900	16	AAQ10542
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ALTERNATIVES

RESULT 1

ID: AAV58451 : standard; DNA: 3383 BP.

AC: AAV58451;

CC: 2501 4598 (first entry)

DF: Modified retinoblastoma tumor suppressor gene.

EW: Modified retinoblastoma tumor suppressor gene. Full protein, correct the tag.

FW: Cellular proliferation inhibitor; ss.

OS: Homo sapiens.

PH: Key Location/Qualifiers

FI: CDS 7..2422

FI: /*tag= a

PN: W9847091-A2.

PP: 27-AUG-1998.

PP: 19-FEB-1998: 98W-0504041.

PP: 20-FEB-1997: 97US-0048118.

PA: (BAYU) HAYLOR COLLEGE MEDICINE.

PA: (TEXA) UNIV TEXAS SYSTEM.

PI: Benedict WF, Hu S, Xu H, Zhou Y.

XX

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 RESULT 4
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 ID AAA29391 standard: DNA: 4889 BP.
 XX AC AAA29391;
 XX
 DI 12-SEP-2000 (first entry)
 XX Human retinoblastoma gene.
 DE
 XX
 KW hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
 KW retinoblastoma; p53; tumour suppressor; inhibitor; after isochlorosis;
 KW proliferation; immortal; tumour therapy; macular degeneration; activator;
 KW INK4; ss
 XX Homo sapiens.
 OS
 XX W0200031248 A2.
 FN
 XX 02-JUN-2000.
 DD
 XX 24-NOV-1999; 99W-0527407.
 PE
 XX 25-NOV-1998; 98OS-0109891.
 PR 17-FEB-1999; 99OS-0120549.
 XX
 PA (GENE:) GENE10CA INC.
 XX
 PI Hannon GJ, Beach DH;

GenCore version 5.1.3
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OM protein nucleic search, using frame_plus.p2n model

Run on: January 16, 2003, 21:41:58 : Search time 273.438 Seconds
(without alignments)
7011.280 Million cell updates/sec

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Perfect score: 4382
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Gapop 6.0, Ygapext 7.0
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Searches: 2185249 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum hit seq length: 0
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Post processing: Minimum Match 0%
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Listing first 40 summaries

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4382	100.0	3323	19	AAV58446
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3	4333	98.9	2994	14	AAO41545
4	4333	98.9	2994	19	AAV40004
5	4333	98.9	2994	21	AAZ43287
6	4333	98.9	2995	20	AAZ90450
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8	4333	98.9	2995	23	AAH34474
9	4333	98.9	2995	23	AAH50904
10	4333	98.9	3555	19	AAV58440
11	4333	98.9	3555	19	AAV54990
12	4333	98.9	4839	21	AAA29391
13	4333	98.9	4839	21	AAZ88444
14	4333	98.9	4839	24	ABL62873
15	4329	98.8	2995	16	AAZ90659
16	4327	98.8	2994	11	AAO04714
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18	4323	98.7	3554	19	AAV58452
19	4318	98.6	2995	16	AAH86398
20	4290	97.9	4740	24	ABK86379
21	4287	97.8	4597	9	AAH81369
22	4286	97.8	4597	15	AAQ70536
23	4283	97.8	4597	20	AAH04501
24	4217	96.2	3266	19	AAV58444
25	4217	96.2	3323	19	AAV58443
26	4217	96.2	3392	19	AAV58442
27	4217	96.2	3455	19	AAV58441
28	4213	96.1	3233	15	AAQ72690
29	4199	95.8	5556	19	AAH53489
30	4192	95.7	3218	19	AAV54991
31	4141	94.5	4579	9	AAH81261
32	4017	91.7	3113	19	AAV58445
33	4007	91.4	3347	19	AAV58448
34	3991	91.1	3377	19	AAV58450
35	3984	90.9	3383	19	AAV58451
36	3683	84.0	3161	19	AAV58449
37	1821	41.6	18403	20	AAH04502
38	1723	39.3	18177	10	AAH90490
39	790	18.0	3960	24	AAH83840
40	789	18.0	4170	24	AAZ94981
41	755	17.3	4853	24	ABK84660
42	754	17.3	2808	13	AAZ62965
43	746	17.0	3249	16	AAH82748
44	626	14.3	3291	23	AAH81193
45	528	12.1	3213	23	ABK12861

ALIGNMENTS

RESULT 1	
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AC	AAV58446;
AC	AAV58446;
DT	02-DEC-1998 (first entry)
XX	Modified retinoblastoma tumor suppressor gene.
DE	Modified retinoblastoma tumor suppressor: RBP protein; cancer therapy.
FW	Cellular proliferation inhibitor, ss.
KW	Homo sapiens.
OS	Homo sapiens.
XX	Key
PH	Location/Qualifiers
FT	CDS
FT	7..2562
FT	/*tag- a

[illegible][illegible]


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35 35 -----ValAspLeuAspGluMetSerPheThrPheThrGluLeu 43
36 36 AICGCGAAGCTTAAATCCAGACAGTACACAGATGAGATGCTGCTTACCTTACTGACCTA 366
37 37 -----GluLysAsnIleLeuSerValIleLysPheAsnLeuLeuLysGluIleAspThr 63
38 38 TACAAAAAATACAAACAGAGTGCATAAATATCTTAATTAATTAATAAAGAAATTCATACC 426
39 39 -----SerThrIysValAspAsnAlaMetSerArgLeuLeuLysIleLysValIlePheAla 83
40 40 AATACAAATTTGATTAATATATATATATATATATATATATATATATATATATATATAT 486
41 41 -----LeuPheSerLysLeuGluArgThrCysGluLeuIleLeuLeuLeuLeuLeuLeuLeu 103
42 42 TCTCTTCAGCAAAATCCAAAGGACATCTCAACTTATATATATATATATATATATATATAT 546
43 43 -----IleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu 123
44 44 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 606
45 45 -----AlaIleLysGluValIleGluMetGluAspAspLeuValIleSerPheGluMetLeu 143
46 46 GTTAAAGAGATATATATATATATATATATATATATATATATATATATATATATATATAT 666
47 47 -----CysValLeuAspLysPheIleLysLeuSerProMetLeuLeuLysGluProTyrLys 163
48 48 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 726
49 49 -----ThrAlaValIleProIleAsnLysSerProArgThrProArgArgGlyGluAsnArgSer 183
50 50 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 786
51 51 -----AlaArgAlaIleLysGluMetGluAsnAspThrArgIleIleGluValLysCysLysGlu 203
52 52 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 846
53 53 -----HisGluThrLysAsnIleAspGluValLysAsnValTyrPheLysAsnProIleLeuPheMet 223
54 54 CATTGAGATATATATATATATATATATATATATATATATATATATATATATATATATAT 906
55 55 -----AsnSerLeuLysLysValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArg 243
56 56 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 966
57 57 -----TyrGluThrIleLysLysAsnLysAspLysAspLysAspLysAspLysAspLysAsp 263
58 58 TACAGAGAAATTTATCTTAAATAAAGATCTAGATGTAAGATTTATTTTGGATCATGAT 1026
59 59 -----CysThrIleGluIleThrAspSerIleAspSerPheGluThrGluArgThrProArgLysSer 283
60 60 AAAAAATCTTCACACACACACACACACACACACACACACACACACACACACACACACACAC 1086
61 61 -----AsnLeuAspLeuValAsnValIleProProIleIleThrProValArgThrValMetAsn 303
62 62 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1146
63 63 -----ThrIleGluThrIleMetMetIleLeuAsnSerAlaSerAspGluProSerGluAsnLeu 323
64 64 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1206
65 65 -----IleSerIyrPheAsnAspCysThrValAsnProLysGluSerIleLeuLysArgValLys 343
66 66 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1266
67 67 -----AspIleGlyTyrIlePheLysGluIleThrPheAlaLysAlaValGlyGluIleCysValGlu 363
68 68 GATATAGGATACATCTTAAACACAAATTTCTTAAAGCTGTGCGACACAGGGTGTGTGCGAA 1326

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364 364 IleGlySerGlnArgTyrLysLeuGlyValArgLeuPheTyrIysArgValMetGluSerMet 483
365 365 TTTTATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1486
366 366 ATTTGATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1486
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368 368 CTTAAATCAGAAGAAGACGATTATCCATTCAAAATTTACCAAACTTCCTCAAIGACAAC 1446
369 369 -----IlePheIleMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 423
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400 400 CCAATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2406
401 401 GlyGlyAsnGluTyrLeuSerProLysSerProTyrLysIleSerGluThrLeuPro 743

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146 240/ GAGAGAAATGATATATTCAGGCTGAAAGTGTATATAAAATTCAGAAAGCTGGCA 2466
 147 744 ThrProThrLysMetThrProArgSerArgLeuValSerIleGlyGlySerPheCly 764
 148 246/ AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2526
 149 764 ThrSerGlyLysPheGlyLysIleAsnGlnMetValLysAsnSerAspArgValLeuLys 784
 150 252/ ACTTCAGAGAGCTGCAAGAAATAAACACAGATGCTGAAAGCAAGCAAGCTGCTCAAA 2586
 151 784 ArgSerAlaGlyLysSerAspProLysProLysProLysLysLeuArgPheAspIleGlu 804
 152 258/ AGAAGTGTGAAGGAAGAAAGCTGCTTAAACACAGCTGAAAGAAAGCTGCTTAAATISAA 2646
 153 804 GlySerAspIleAlaAspGlySerLysHisSerProGlyGlySerLysPheGlnIleLys 824
 154 264/ GAATACATGAGAGATGAGAAATTAACATCTGCGAGAGAGCTCAAAATTCAGAGAAA 2706
 155 824 LeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 844
 156 270/ CTGGTACAAAAGATCTCTTACCTGAAACAGCAATGCAAAAGCAGAAAATCAATGATGCA 2766
 157 844 AspThrSerAsnGlySerLysLys 851
 158 276/ GATACCTCAACAGAGAGAGAGAAA 2790

643011 11
 159 AAV54990
 160 AAV54990 standard; DNA: 4555 bp.

161 AAV54990;
 162 26 NOV 1998 (first entry)

163 DNA sequence of the specification.

164 Minimal promoter: tetacycline responsive expression vector; TREV;
 165 transcriptional transactivator domain; 11b;
 166 tetacycline repressor protein; 18b; tetacycline operator;
 167 production: stable cell line; protein production;
 168 tumour suppressor protein; treatment: cancer; ss.

169 Unidentifed.

170 Key location/qualifiers
 171 CDS 7..2794
 172 FT /*aaq- a

173 EN W09807185 A2.

174 27 AUG 1998.

175 19 FEB 1998; 98W0 0804092.

176 20 FEB 1997; 970S 0048755.

177 (EPXA) UNIV TEXAS SYSTEM.

178 Hu S. Lopezheis CJ, Xu H, Zhou Y;

179 WPT: 1998 480746/41.

180 P-504; AAW71454.

181 New tetacycline responsive expression vectors used for the
 182 tightly controlled expression of genes, such as tumour suppressor
 183 genes for treating cancers

184 Disclosure: Pages 145-150; 190pp; English

185 The present sequence appears in the specification, which describes a
 186 tetacycline responsive expression vector (TREV), which contains a
 187 sequence encoding a fusion protein comprising a transcriptional

188 transactivation domain (TIP) operatively attached to a tetacycline
 189 repressor protein (TRP), the first sequence operatively positioned
 190 downstream of a promoter, the vector also contains a cloning site
 191 operatively positioned downstream of a basal promoter comprising a
 192 tetacycline operator, the TRPs can be used to produce stable cell
 193 lines in which gene expression is tightly regulated by tetacycline.
 194 They can be used for the production of proteins such as tumour
 195 suppressor proteins which can be used for treating diseases characterised
 196 by abnormal cellular proliferation, particularly cancers.

197 Sequence 3555 bp; 1171 A; 584 C; 653 G; 1047 T; 0 other;

198 Alignment Scores:

199 Pred. No.: 0 Length: 4555
 200 Score: 4333.50 Matches: 851
 201 Percent Similarity: 91.70% Conservatave: 0
 202 Best Local Similarity: 91.70% Mismatches: 0
 203 Query Match: 98.89% Indels: 77
 204 DB: 19 Gaps: 1

205 US-09-026-459A-39 (1-851) x AAV54990 (1-3555)

206 QY 1 MetProThrLysThrProArgLysThrArgAlaAlaThrAlaAlaAlaAlaAlaAlaPro 20
 207 Db 7 ATGGCGGCTCAAAAACGAGGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 66
 208 QY 21 ProAlaProProProProProProProProProProProProProProProProPro 30
 209 Db 67 CCGGCACG 126
 210 QY 30 -----ValAspLeuAspGlnMetSerPheThrThrThrGluLeu 40
 211 Db 127 GACCTGCTCTCTGCTCAGGCTTCAGCTTTTGAACAACACAGACAACTGCATTTATTCAT 186
 212 QY 30 -----TGTGAGAAATTAAGATACAGATCATGTACAGACAGAGAGTTTGTTTAAATTTC 30
 213 Db 187 TGTGAGAAATTAAGATACAGATCATGTACAGACAGAGAGTTTGTTTAAATTTCGAGAAA 246
 214 QY 30 -----TGTGAGAAATTAAGATACAGATCATGTACAGACAGAGAGTTTGTTTAAATTTC 30
 215 Db 247 GTTTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 306
 216 QY 31 -----ValAspLeuAspGlnMetSerPheThrThrThrGluLeu 40
 217 Db 307 AATGCTATCTTTATTCGAGAGAGTTCAGCTTACAGATGCTGCTGCTGCTGCTGCTGCTG 366
 218 QY 44 GlnLysAsnIleGluIleSerValHisLysPheAsnLeuLeuLysGlnIleAspThr 63
 219 Db 367 CAGAAAAACATAGAAATCAGTGTCCATTAATCTTTTAACTTAACTTAACTTAACTTAACT 426
 220 QY 64 SerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysLysLysLysLysLysLys 83
 221 Db 427 AGTACCAAGTTCATAAGCTATCTCAAGACCTGCAAGCAAGCAAGCAAGCAAGCAAGCA 486
 222 QY 84 LeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrThrGlnProSerSer 103
 223 Db 487 CTTTCAGCAAAATTCGAAAGAGACATGAGACCTTATATATTTGACAAACCTGAGCTTC 546
 224 QY 104 IleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu 123
 225 Db 547 ATATCTATCGAAATTAATTCGATTGCTCTAAATTTCTTGGATCTCATTTTATTTATTA 606
 226 QY 124 AlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheThrThrGlnPro 143
 227 Db 607 GCTAAAGGGAAGCTATACAAATGGAAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 666
 228 QY 144 CysValLeuAspThrPheLeuLysLeuSerProProMetLeuLeuLysLysLysLysLys 163
 229 Db 667 TGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
 230 QY 164 ThrAlaValIleProLysAsnGlySerProArgThrProArgArgGlyGlnAsnArgSer 183
 231 Db 727 ACAGCTTTATACGCTTAATGCTTACCTGCAACACAGGAGAGAGAGAGAGAGAGAGAG 786

259 GACCTGGCTTGGTCAAGCTTGGATTTCAGAAAGAACAAAGAACCTGATTTTATATGCTATTA 318
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 449 AATGCTATCTTATGGAGAGCTGAGCTAGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 498
 44 GlnAspAsn100uThrProSerValHisLysPhePheAsnLeuLeuLysGluLeuAspThr 63
 499 CAGAAAGAAATAGAAATCACTGCTATTAATCTTTAACTTAAAGAAATATATAGC 558
 64 SerThrLysValAspAsn100uMetSerArgLeuLeuLysLysTyrAspValLeuPheAla 83
 559 ACTATCAAACTGATAAATCTATGCTAAAGCTGCTGAGAAAGTATGATGATGATGATGATGATG 618
 84 LeuPheSerLysLeuGluArgThrCysGluLeuLeuLeuThrGluThrGluProSerSerSer 103
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 124 AlalysylGluValLeuGluMetGluAspLeuValLeuSerPheGluLeuMetLeu 143
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 144 CysValLeuAspTyrPheLeuLysLeuSerProProMetLeuLeuLysGluProTyrLys 163
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Gapcore version 5.1.1
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CM nucleotide nucleotide search, using SW model

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Searched: 219529 seqs, 112569419 residues

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21:	/SIDS2/quadat/geneseq/emb1/NA2000.DAT:*	
22:	/SIDS2/quadat/geneseq/emb1/NA2001.DAT:*	
23:	/SIDS2/quadat/geneseq/emb1/NA2002.DAT:*	
24:	/SIDS2/quadat/geneseq/emb1/NA2003.DAT:*	

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Quality	Match	Length	DB	ID	Description
1	3323	100.0	3323	19	AAV58446		Modified retinobla
2	3226	97.1	3226	19	AAV58447		Modified retinobla
3	3226	97.1	3226	19	AAV58444		Modified retinobla
4	3226	97.1	3323	19	AAV58443		Modified retinobla
5	3226	97.1	3323	19	AAV58442		Modified retinobla
6	3226	97.1	3323	19	AAV58441		Modified retinobla
7	3226	97.1	3323	19	AAV58440		Modified retinobla
8	3226	97.1	3323	19	AAV58439		Modified retinobla
9	3226	97.1	3323	21	AAA29391		Human retinoblasto

10	3226	97.1	4839	21	AAV58444	Human androgen re
11	3226	97.1	4839	24	AAH62873	Breast cancer rela
12	3224	97.0	4597	9	AAH81169	Human retinoblasto
13	3224	97.0	4597	15	AAQ70546	Human retinoblasto
14	3224	97.0	4597	20	AAQ04501	Human retinoblasto
15	3222	97.0	4594	19	AAV58452	Modified retinobla
16	3212	96.7	3233	15	AAQ72690	Modified retinobla
17	3212	96.7	3218	19	AAV54991	RNA sequence of th
18	3194	96.1	4740	24	AAH86079	Human retinoblasto
19	3148	94.7	4579	9	AAH82261	Probe for retinobl
20	3107	93.5	3113	19	AAV58445	Modified retinobla
21	3066	92.3	3317	19	AAV58448	Modified retinobla
22	2945	88.6	5056	10	AAV90489	cDNA of human ret
23	2867	86.3	3383	19	AAV58451	Modified retinobla
24	2855	85.9	3377	19	AAV58450	Modified retinobla
25	2827	85.1	3161	19	AAV58449	Modified retinobla
26	2534	76.3	2594	11	AAQ04713	Cancer suppressin
27	2534	76.3	2594	14	AAQ11545	Retinoblastoma gen
28	2534	76.3	2594	19	AAV40004	Retinoblastoma pro
29	2534	76.3	2594	21	AAZ40287	Wild type human re
30	2531	76.2	2595	20	AAV90450	Human p110 RB ret
31	2531	76.2	2595	20	AAV90450	cDNA encoding a re
32	2531	76.2	2595	22	AAH25755	Retinoblastoma tum
33	2531	76.2	2595	22	AAH25755	Retinoblastoma tum
34	2531	76.2	2595	23	AAH50904	Retinoblastoma tum
35	2529	76.1	2595	16	AAQ90059	Retinoblastoma tum
36	2524	76.0	2595	16	AAQ86398	Human Rb110 cDNA
37	845	25.1	18303	20	AAV04502	Human retinoblasto
38	831	25.0	18177	10	AAV90490	DNA of human retin
39	220	6.6	1698	18	AAH62190	Antisense sequenc
40	220	6.6	1832	18	AAH62191	Direct tandem repe
41	220	6.6	2634	18	AAH62194	Construct pMK10/AS
42	220	6.6	3453	18	AAH62193	Construct pMK10/AS
43	220	6.6	3453	18	AAH62196	Construct pMK10/AS
44	218	6.6	999	16	AAH11542	Retinoblastoma pro
45	218	6.6	1697	16	AAH101541	Retinoblastoma pro

ALIGNMENTS

RESULT 1

AAV58446
ID: AAV58446 standard; DNA: 3323 bp.

XX AAV58446:
XX 62-DEC-1998 (first entry)

XX 62-DEC-1998 (first entry)

XX Modified retinoblastoma tumour suppressor gene.

XX Modified retinoblastoma tumour suppressor: RTSP protein; cancer therapy;
cellular proliferation inhibitor; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 7..2562

XX FT /*taq- a

XX W09847091-A2.

XX 27-AUG-1998.

XX 19-FEB-1998; 98WO-0504041.

XX 20-FEB-1997; 97US 0038118.

XX (BAYLOR COLLEGE MEDICINE,
TEXAS) UNIV TEXAS SYSTEM.

XX Benedict WF, Hu S, Xu H, Zhou Y;

XX

XX
Sequence 3461 BP; 1141 A; 675 C; 627 G; 1018 T; 0 other;

Query Match: 97.14; Score: 3228; DB: 19; Length: 3461;
Best Local Similarity: 100.0%; Pred. No.: 0;

[illegible]

Db 1442 TTTTGAATGTCAGACAGATTTGCTTTTCCCATGAGATTCGTAATGCTTAAATTTAAAGC 1481
 QY 1360 GTTTCGATTTTACAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1409
 Db 1482 GTTTCGATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1541
 QY 1410 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1469
 Db 1542 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1601
 QY 1470 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1529
 Db 1602 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1661
 QY 1540 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1589
 Db 1662 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1721
 QY 1590 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1649
 Db 1722 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1781
 QY 1650 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1709
 Db 1782 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1841
 QY 1710 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1769
 Db 1842 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1901
 QY 1770 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1829
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 QY 1830 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1889
 Db 1962 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2021
 QY 1890 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 1949
 Db 2022 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2081
 QY 1950 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2009
 Db 2082 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2141
 QY 2010 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2069
 Db 2142 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2201
 QY 2070 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2129
 Db 2202 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2261
 QY 2130 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2189
 Db 2262 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2321
 QY 2190 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2249
 Db 2322 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2381
 QY 2250 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2309
 Db 2382 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2441
 QY 2310 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2369
 Db 2442 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2501
 QY 2370 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2429

Db 2502 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2561
 QY 2430 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2489
 Db 2562 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2621
 QY 2490 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2549
 Db 2622 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2681
 QY 2550 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2609
 Db 2682 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2741
 QY 2610 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2669
 Db 2742 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2801
 QY 2670 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2729
 Db 2802 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2861
 QY 2730 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2789
 Db 2862 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2921
 QY 2790 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2849
 Db 2922 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2981
 QY 2850 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2909
 Db 2982 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3041
 QY 2910 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 2969
 Db 3042 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3101
 QY 2970 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3029
 Db 3102 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3161
 QY 3030 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3089
 Db 3162 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3221
 QY 3090 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3149
 Db 3222 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3281
 QY 3150 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3209
 Db 3282 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3341
 QY 3210 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3269
 Db 3342 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3401
 QY 3270 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3329
 Db 3402 AATGATATAAAATTTTAAAGTCAAGAGTCTTATCAAACTCAAGGCACTGACCAACAGA 3461

RESULT 7

AAV58440

ID AAV58440 standard: DNA; 3555 BP.

XX AAV58440;

AC AAV58440;

QY 02-DEC-1998 (first entry)

XX Modified retinoblastoma tumour suppressor gene.

DE

XX

[illegible]


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18 2072 GCTGCTTCACTGGTTTATAAAAAAGGCTATGCGGTACGCTACGCTCCGCTAAATACACT 2131
19 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 1829
20 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2191
21 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 1889
22 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2251
23 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 1949
24 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2311
25 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2009
26 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2371
27 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2069
28 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2431
29 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2129
30 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2491
31 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2189
32 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2551
33 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2249
34 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2611
35 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2309
36 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2671
37 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2569
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39 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2429
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41 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2489
42 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2851
43 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2549
44 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2911
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46 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2971
47 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2669
48 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 3031
49 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2729
50 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 3091
51 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2789
52 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 3151
53 TTTTGGTAAAGGTTCTGCTGAGTACCGCAGAAATAGAACATATCATCTGAGCCCTTTTCCA 2849

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18 3152 TTTTAAAAAGTTGAGCAGATTGTTTCTCTCCCAAGTAAAAATGCGTGTCTTTATGGAT 3211
19 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 2909
20 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3271
21 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 2969
22 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3331
23 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3029
24 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3391
25 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3069
26 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3451
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29 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3209
30 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3571
31 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3269
32 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3641
33 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3321
34 ACTAAGTAATATATTTTAAAGTGGAGTATTTTAAATGGAAGGATGTTGATCTATTCTTTT 3685

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RESULT 12

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AANB1369
ID AANB1369 standard; DNA; 4597 BP.
XX AANB1369;
XX AC
XX 22-OCT 1990 (first entry)
XX Human retinoblastoma gene.
XX Retinoblastoma; neoplasm; osteosarcoma; ss.
XX Homo sapiens.
XX Key location/Qualifiers
XX CDS 337..2787
XX FT /*tag- a
XX EN BP259031-A.
XX
XX 09-MAR-1988.
XX 11-AUG-1987; 87EP-0307095.
XX 11-AUG-1986; 86US-0895163.
XX
XX (MASS-) MASSACHUSETTS EYE.
XX (WHIT-) WHITEHEAD INST BIOMED RE.
XX Dryja TP, Friend S;
XX WPL; 1988-065827/10.
XX p-PSDB; AAP82112.
XX
XX Diagnosis of retinoblastoma - using genetic material corresp. to a normal
XX human retinoblastoma gene or a unique sub-region
XX
XX Disclosure; / p; English.
PS

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this gene encodes a protein, the absence of which is associated with a
 malignancy. It is used to produce an antibody to the protein containing
 this with the tumour sample and detecting immune complexes as indication
 of the presence in the tumour sample of the protein. Whole sequence of
 a unique sub-region can be used. The method identifies patients lacking
 the defective retinoblastoma (rb) allele and thus are not at risk of
 developing the disease.

Sequence 497 BP; 1489 A; 839 C; 815 G; 1454 T; 0 other; XX

[illegible][illegible]

07 2736 ACTTCAAAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 2789
11 2961 ACTTCAAAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3020
07 2790 TTTAAAAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 2849
11 3021 TTTAAAAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3080
07 2800 ATATCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 2909
11 3081 ATATCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3140
07 2910 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 2969
11 3141 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3200
07 2920 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3029
11 3201 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3260
07 3030 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3089
11 3261 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3320
07 3090 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3149
11 3321 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3380
07 3150 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3209
11 3381 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3440
07 3210 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3269
11 3441 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3500
07 3270 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3329
11 3501 TTTTGTAGTCAATGTTAGTCAATGTTATTTATACAGATTGCAAAATCTGTGTGTTAAATCTCTGCCA 3554

Sort file completed: January 16, 2003, 23:37:43
File size: 455,847 bytes

GenCore version 5.1.4
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CM nucleic acid search, using SW model

Run on: January 16, 2003, 15:20:17 : Search time 406.018 Seconds
(without alignments)
17541.794 Million cell updates/sec

Filter: OS 09-026-459A 44

Perfect score: 4161
Sequence: 1 CAGGCAAGCGGCTGTAAGAAAC.....AAAGAGCAATATGATAGT 3161

Scoring table: IDENTITY_NP

Gapop 10.0, Gapext 1.0

Searches: 2185249 seqs, 1176990159 residues

Total number of hits satisfying chosen parameters: 4 (70478)

Minimum db seq length: 0

Maximum db seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 8 Geneseq.101002.*

Result No.	Score	Match	Length	db ID	Description
1	4161	100.0	4161	AAV58449	Modified retinobla
2	2965	93.8	3347	AAV58448	Modified retinobla
3	2945	92.9	3377	AAV58450	Modified retinobla
4	2827.4	89.4	4113	AAV58445	Modified retinobla
5	2827.4	89.4	4218	AAV54951	DNA sequence of th
6	2827.4	89.4	4266	AAV58444	Modified retinobla
7	2827.4	89.4	4323	AAV58446	Modified retinobla
8	2827.4	89.4	4323	AAV58446	Modified retinobla
9	2827.4	89.4	4392	AAV58442	Modified retinobla

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	db ID	Description
1	4161	100.0	4161	AAV58449	Modified retinobla
2	2965	93.8	3347	AAV58448	Modified retinobla
3	2945	92.9	3377	AAV58450	Modified retinobla
4	2827.4	89.4	4113	AAV58445	Modified retinobla
5	2827.4	89.4	4218	AAV54951	DNA sequence of th
6	2827.4	89.4	4266	AAV58444	Modified retinobla
7	2827.4	89.4	4323	AAV58446	Modified retinobla
8	2827.4	89.4	4323	AAV58446	Modified retinobla
9	2827.4	89.4	4392	AAV58442	Modified retinobla

10	2827.4	89.4	3455	19	AAV58441	Modified retinobla
11	2827.4	89.4	3461	19	AAV58447	Modified retinobla
12	2827.4	89.4	3554	19	AAV58452	Modified retinobla
13	2827.4	89.4	3555	19	AAV58440	Modified retinobla
14	2827.4	89.4	3555	19	AAV54950	DNA sequence of th
15	2827.4	89.4	4849	21	AAV54951	Human retinoblasto
16	2827.4	89.4	4849	21	AAV58444	Human androgen res
17	2827.4	89.4	4849	24	AHL62873	breast cancer rela
18	2825.8	89.4	4597	9	AAH1369	Human retinoblasto
19	2825.8	89.4	4597	15	AAH07056	Human retinoblasto
20	2825.8	89.4	4597	20	AAH04501	Human retinoblasto
21	2819.4	89.2	4743	24	AHR86079	Human retinoblasto
22	2814.8	89.0	3233	15	AAG72690	Retinoblastoma 94K
23	2769	87.6	5056	10	AAH90489	cDNA of human ret
24	2766	87.5	4579	9	AAH81261	probe for retinobl
25	2757.4	87.2	3484	19	AAV58451	Modified retinobla
26	2135.4	67.6	2994	11	AAH04714	Cancer suppressin
27	2135.4	67.6	2994	14	AAH1545	Retinoblastoma qm
28	2135.4	67.6	2994	19	AAH40004	Retinoblastoma pro
29	2135.4	67.6	2994	21	AAH43287	Wild type human re
30	2132.4	67.5	2995	20	AAH90450	Human p110 RB ret
31	2132.4	67.5	2995	20	AAH00747	cDNA encoding a re
32	2132.4	67.5	2995	22	AAH25765	Retinoblastoma tum
33	2132.4	67.5	2995	22	AAH04474	Retinoblastoma tum
34	2132.4	67.5	2995	23	AAH50904	Retinoblastoma tum
35	2132.2	67.5	2995	16	AAH86498	Human Rb110 cDNA
36	2130.8	67.4	2995	16	AAH90059	Retinoblastoma tum
37	835	26.4	18303	20	AAH04502	Human retinoblasto
38	831.8	26.3	18177	10	AAH90490	DNA of human retin
39	220.8	7.0	1698	18	AAH62496	Antisense sequence
40	220.8	7.0	1698	18	AAH62491	Direct tandem repe
41	220.8	7.0	2143	18	AAH62491	5'end of pRb110AS
42	220.8	7.0	3493	18	AAH62491	5'end of pRb110AS
43	220.8	7.0	3673	18	AAH62491	5'end of pRb110AS
44	218.8	6.9	900	16	AAH91542	Retinoblastoma pro
45	218.8	6.9	1647	16	AAH91541	Retinoblastoma pro

ALIGNMENTS

RESULTS

AAV58449 standard: DNA: 4161 BP.

AAV58449;

02-DEC-1998 (first entry)

Modified retinoblastoma tumour suppressor gene.

Modified retinoblastoma tumour suppressor, RbSE protein, cancer therapy;
cellular proliferation inhibitor, ss.

Homo sapiens.

Key Location/Qualifiers

CDS 7..2400

FT /tag- a

XX M09837091-A2.

XX 27-AUG-1998.

XX 19-FEB-1998; 98W0-050041.

XX 20-FEB-1997; 97US-0048118.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Benedict WF, Hu S, Xu H, Zhou Y;

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1419 CAGGATTTGATGAGTTAAATTTAAAGGCTTTGATTTTACAAAATGATGAGAAAGTT 1378
 1427 TATTAAGGACAAAGGAAATTCACAAAGCAAAATGATAAATAATAGAACATGGAAC 1276
 1435 TATTAAGGACAAAGGAAATTCACAAAGCAAAATGATAAATAATAGAACATGGAAC 1438
 1443 TATTAAGGACAAAGGAAATTCACAAAGCAAAATGATAAATAATAGAACATGGAAC 1438
 1451 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 1336
 1459 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 1498
 1467 AATTAAGGACAAAGGAAATTCACAAAGCAAAATGATAAATAATAGAACATGGAAC 1396
 1475 AATTAAGGACAAAGGAAATTCACAAAGCAAAATGATAAATAATAGAACATGGAAC 1558
 1483 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 1456
 1491 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 1618
 1499 AATTAAGGACAAAGGAAATTCACAAAGCAAAATGATAAATAATAGAACATGGAAC 1516
 1507 AATTAAGGACAAAGGAAATTCACAAAGCAAAATGATAAATAATAGAACATGGAAC 1678
 1515 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 1576
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 1579 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 1816
 1587 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 1978
 1595 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 1876
 1603 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 2038
 1611 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 1936
 1619 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 2098
 1627 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 1996
 1635 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 2158
 1643 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 2056
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 1699 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 2398
 1707 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 2296
 1715 ATGAAATATGAGATGCTTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 2458

2297 CCAAAATTTCAAGGAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 2356
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 2597 CCAAAATTTCAAGGAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 2656
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 2999 GTGACAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTTATTTATTAAC 3058
 2897 AATTAAGGACAAAGGAAATTCACAAAGCAAAATGATAAATAATAGAACATGGAAC 2956
 3059 AATTAAGGACAAAGGAAATTCACAAAGCAAAATGATAAATAATAGAACATGGAAC 3118
 2957 TATTAATTTCAAGGAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 3016
 3119 TATTAATTTCAAGGAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 3178
 3017 TATTAATTTCAAGGAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 3076
 3179 TATTAATTTCAAGGAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 3238
 3077 CCAAAATTTCAAGGAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 3136
 3239 CCAAAATTTCAAGGAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 3298
 3137 TATTAATTTCAAGGAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 3196
 3299 TATTAATTTCAAGGAAATTTGATGAGCTCTTATGATGAGCTTTATTTATTTATTAAC 3358

RESULT 9

AAV58442 standard: DNA: 3342 bp.

AAV58442:

02-DEC-1998 (first entry)

Modified retinoblastoma tumour suppressor gene.

Modified retinoblastoma tumour suppressor. RTSP protein. same therapy.

cellular proliferation inhibitor; ss.

Homo sapiens.

Key Location/Qualifiers

7...2641

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W. 1981-2091-A2.

2017-1998

14-00000-1448-98W0-11503041

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REV. 1000-700-11

996087-111-1
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for melanoma suppressor protein with N terminal modification - inhibiting cellular proliferation, particularly cancer

Abstract. We study the asymptotic behavior of the eigenvalues of the Laplacian on a domain in the plane as the boundary curvature goes to infinity. The eigenvalues are ordered by increasing magnitude and we show that they approach those of the Dirichlet problem on a half-plane. This result is proved by studying the asymptotic behavior of the Green's function of the Laplacian on a domain in the plane as the boundary curvature goes to infinity. The Green's function is shown to approach the Green's function of the Dirichlet problem on a half-plane. This result is proved by studying the asymptotic behavior of the Green's function of the Laplacian on a domain in the plane as the boundary curvature goes to infinity. The Green's function is shown to approach the Green's function of the Dirichlet problem on a half-plane.

Claim 22: Page 150-155, 249pp, English.

This sequence encodes a modified retinoblastoma tumour suppressor protein (RbSP) of the invention. The proteins can be used for inhibiting cellular proliferation, when coadministered with a p53 protein. The RbSPs can be used for treating diseases characterised by abnormal cellular proliferation, particularly cancers. The RbSPs have a broader spectrum of activity than wild type RbSPs.

activity than with type A1B2.

Sequence 3392 BP; 1137 A; 614 C; 607 G; 1034 T; 0 other;

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or, Match 89.4%; Score 2827.4; LB 19; Length 3392;

Local Similarity 99.68, Pred. No. 0,

548 TCAAGAAACATATAAACAG^{5'}TGTATACGATTAA[illegible]

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1976-1977

[illegible]

GG CAGGTCCTTCTGTAACGAGAACTTATCTTAAAAATAAAGATTTAGATGTAACA 879

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548 TATTTTCTGGATCATGATATAGACAGTTTGGAAACACAGA 907

677 GAAATGACCTAAATCTTATGAAAGAGGGAATGTAATGCTTCCACACACTCCAG / 36

508 G A A C A C C A C G A A A A A A G T A A C C T T C A T G A A G A G G G A A T G T A A T T C C C A C A C A C A T C C A G 567

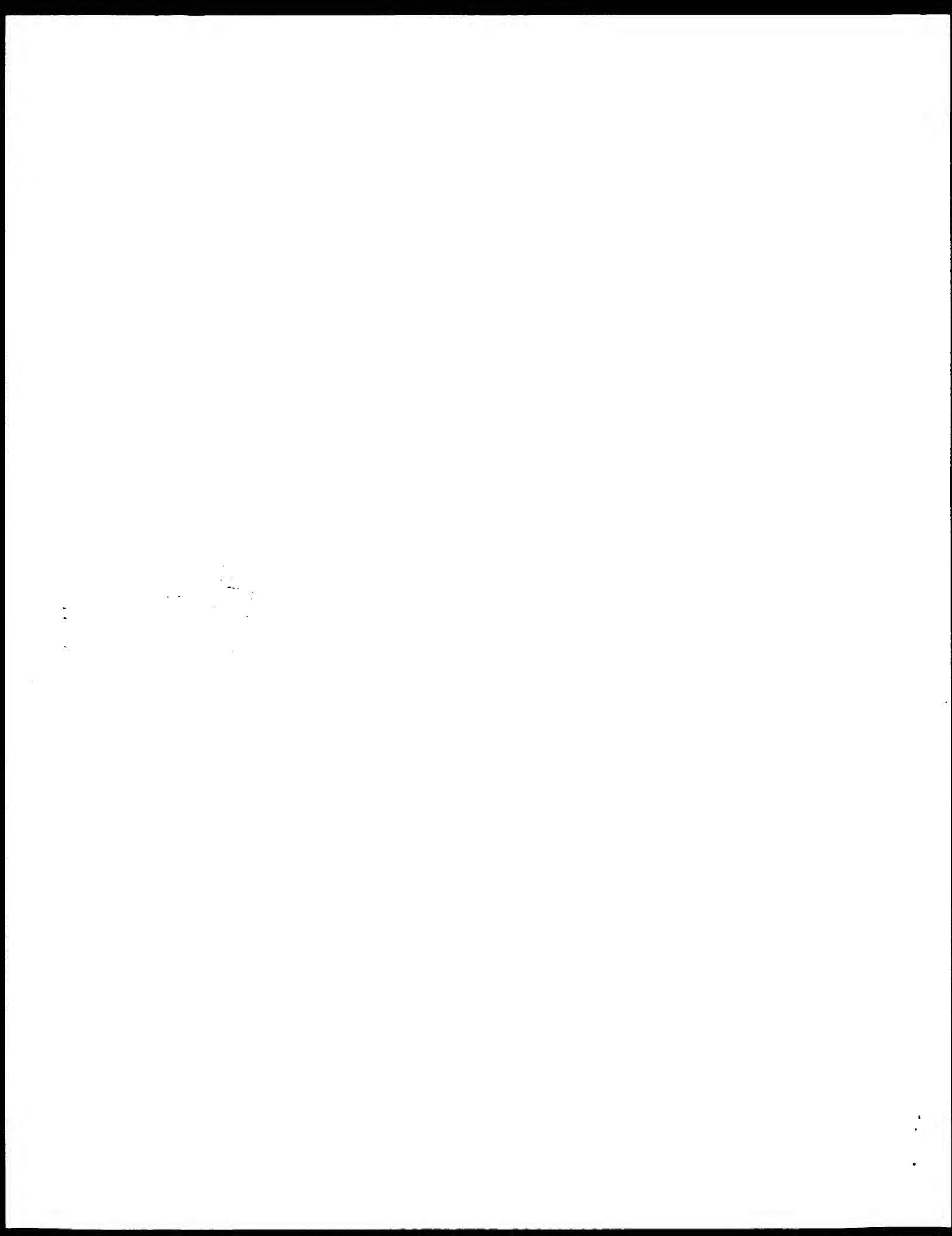
737 TTAGGATGGTATGAACACTATCCAAACAATTAATGATGATTTTAAATTTCAGCAAGTGATC 796

458 TTAGGACGCTATGAACACATAACCAACAATTAAATCATCATTTTAAATTCACCAACGATC 102

1000 AAATTTCGATGAGAAATATTTTTCATATATGCTTTATATGGGTTGGGCTCTGAGGTGTGTA 1396
1001 GAGGCAATATAGCAAGATGACATCTCAGAACTTGATCTCGACACAGATCTGGTTTCCC 1456
1002 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1456
1003 TGGGCAATATAGCAAGATGACATCTCAGAACTTGATCTCGACACAGATCTGGTTTCCC 1456
1004 CATGATTTTGAATGTGCTTAATTTTAAAGGCTTTGATTTTACAAAGTATGATGATGAT 1216
1005 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1516
1006 CAGGATCTGAAAGTCTTAAATTTAAAGGCTTTGATTTTACAAAGTATGATGATGAT 1516
1007 TATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1276
1008 TATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1576
1009 TATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1576
1010 ATCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1336
1011 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1636
1012 ATCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1636
1013 AATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1396
1014 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1696
1015 AATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1696
1016 CTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1456
1017 CTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1756
1018 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1516
1019 AATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1816
1020 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1816
1021 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1576
1022 CTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1876
1023 ATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1636
1024 ATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1936
1025 AATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1696
1026 AATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1936
1027 TATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1816
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1029 TATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1876
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1033 TATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1996
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1178 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2536
1179 GGCACCTGCTGCTCTCAAAAGAACTGCTGAGGAAAGCAACCTCTCTAAATTAATTAAGAAAC 2536
1180 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2296
1181 TATGCTTTTCTATTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2596
1182 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2596
1183 TATGCTTTTCTATTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2356
1184 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2656
1185 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2416
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1190 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2836
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1195 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2716
1196 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3016
1197 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2776
1198 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3076
1199 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2836
1200 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2936
1201 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2956
1202 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 4256
1203 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3016
1204 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3336
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1208 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3136
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1210 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3136
1211 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3436
1212 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3161
1213 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3461
1214 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3161
1215 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3461

RESULT 12
AAV58452
ID AAV58452 standard; DNA; 3554 bp.



Genature version 5.1.4
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0M protein nucleic search, using frame_plus_p2n model

Run on: January 16, 2003, 23:41:58 | Search time 255.994 Seconds
(without alignments)
7011.280 Million cell updates/sec

File: us_09_026_459a_45
Perfect score: 4144
Sequence: 1 MPPKTRKTAATAAAAAA.....TRMKQKNDMSGTSNKEEK 797

Scoring table:
Kgap 10.0, Xgap 0.5
Ygap 10.0, Ygap 0.5
Egap 6.0, Egap 7.0
Igap 6.0, Del 7.0

Searched: 2185249 seqs, 112599959 residues

Total number of hits satisfying chosen parameters: 4376478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

Model: frame_plus_p2n model -dev x86
DB: Geneseq1000000 -fpm -lastap -suffix -r -minmatch 0.1 -lowp2n
Lowp2n -0 -units -bits -start 1 -end 1 -matrix -blossum62 -trans -human40 -cdi
List -45 -dualalign -200 -thp -score -pct -thp_max 100 -thp_min 0 -align 15
Mode: local outfmt pto -norm -ext -hpa -size 500 -minlen 0 -maxlen 2000000000
USR -0500000000 -45 -seqn 1 -252 -45 -mat 1521475229 -ncp 0 -6 -cpg 3
No index -N -lmap -lap -query -neg -score 0 -wait -con 000 -dev -timeout 120
Warn time out -40 -thp -0 -thp -1 -xgap 10 -xgapext 0.5 -fgap 6 -fgapext 7
Ygap 10 -ygapext 0.5 -del 6 -delx 7

Database: Geneseq1000000

1: /SUS2/seqdata/geneseq/geneseq-emb1/NA1987.DAT**
2: /SUS2/seqdata/geneseq/geneseq-emb1/NA1988.DAT**
3: /SUS2/seqdata/geneseq/geneseq-emb1/NA1989.DAT**
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22: /SUS2/seqdata/geneseq/geneseq-emb1/NA2008.DAT**
23: /SUS2/seqdata/geneseq/geneseq-emb1/NA2009.DAT**
24: /SUS2/seqdata/geneseq/geneseq-emb1/NA2010.DAT**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4144	100.0	3161	19	AAV58449	Modified retinobla
2	4103	99.0	3347	19	AAV58448	Modified retinobla
3	4098	98.9	3377	19	AAV58450	Modified retinobla
4	4068.5	98.2	2994	14	AAQ41545	Retinoblastoma gen
5	4068.5	98.2	2994	19	AAV40004	Retinoblastoma pro
6	4068.5	98.2	2994	21	AAZ40287	Wild type human re
7	4068.5	98.2	2995	20	AAZ90350	Human p10 RB ret
8	4068.5	98.2	2995	22	AAH25755	Retinoblastoma tum
9	4068.5	98.2	2995	22	AAH04474	Retinoblastoma tum
10	4068.5	98.2	2995	23	ABH50904	Retinoblastoma tum
11	4068.5	98.2	3554	19	AAV58452	Modified retinobla
12	4068.5	98.2	3555	19	AAV58440	Modified retinobla
13	4068.5	98.2	3555	19	AAV54390	DNA sequence of th
14	4068.5	98.2	4839	21	AAZ29351	Human retinoblasto
15	4068.5	98.2	4839	21	AAZ88444	Human androgen rec
16	4068.5	98.2	4839	24	ABH62873	Human cancer rela
17	4064.5	98.1	2995	16	AAQ90059	Retinoblastoma tum
18	4060.5	98.0	2995	16	AAQ86398	Human Rb10 cDNA
19	4059.5	98.0	2994	11	AAQ04713	Cancer suppressing
20	4059.5	98.0	2995	20	AAQ00737	cDNA encoding a re
21	4057.5	97.9	4740	24	ABH86079	Human retinoblasto
22	4006	96.7	4597	15	AAQ70536	Human retinoblasto
23	4003	96.6	4597	20	AAQ04501	Human retinoblasto
24	4002	96.6	4597	9	AAH81369	Human retinoblasto
25	3912	94.4	3461	19	AAV58447	Modified retinobla
26	3902.5	94.2	4579	9	AAH81261	Probe for retinobl
27	3880.5	93.6	3455	19	AAV58441	Modified retinobla
28	3845	92.8	5056	10	AAH90489	cDNA of human reti
29	3799	91.7	3383	19	AAV58451	Modified retinobla
30	3770.5	91.0	3392	19	AAV58442	Modified retinobla
31	3683	88.9	3323	19	AAV58446	Modified retinobla
32	3638.5	87.8	3323	19	AAV58443	Modified retinobla
33	3550	85.7	3113	19	AAV58445	Modified retinobla
34	3550	85.7	3218	19	AAV54991	DNA sequence of th
35	3550	85.7	3233	15	AAQ72690	Retinoblastoma 94K
36	3550	85.7	3266	19	AAV58444	Modified retinobla
37	1655.5	39.9	18303	20	AAQ04502	Human retinoblasto
38	1578.5	38.1	18177	10	AAH90490	DNA of human retin
39	720.5	17.4	3960	24	ABH84840	Human cDNA differe
40	719.5	17.4	4130	24	AAH94481	Human cDNA differe
41	712.5	17.2	4853	24	ABH84660	Sealys complete pl
42	709.5	17.1	808	13	AAZ52005	pR2 retinoblastom
43	669	16.1	3249	16	AAH82748	Human retinoblasto
44	578	13.9	3291	23	AAH84393	Human retinoblasto
45	516.5	12.5	3747	19	AAV05714	Human retinoblasto

ALIGNMENTS

RESULT 1
ID: AAV58449 Standard: DNA: 3161 bp.
AC: AAV58449;
DT: 02-DEC-1998 (first entry)
ID: Modified retinoblastoma tumour suppressor gene.
XX: Modified retinoblastoma tumour suppressor; FTSP protein; cancer therapy;
KW: Cellular proliferation inhibitor; ss.
QS: Homo sapiens.
XX: Key Location/Qualifiers
FH CDS 7..2400
FT /*tag= a

XX
PN W-037691-A2.
XX
PD 27 AUG 1998.
XX
PR 19 FEB 1998; 98W0-US03041.
XX
PR 20 FEB 1997; 97US-0038118.
XX
PA (BAYD) BAYLOR COLLEGE MEDICINE,
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Benedict WF, Hu S, Xu H, Zhou Y;
XX PR WFS: 1998-480788/41.
XX PR PVSDB: AAW69473.
XX
PI Retinoblastoma suppressor protein with N-terminal modification -
XX PI inhibiting cellular proliferation, particularly cancer
XX
XX Claim 23: Page 293, 297; 24pp. English.
XX
XX This sequence encodes a modified retinoblastoma tumour suppressor
XX protein (RTPSP) of the invention. The proteins can be used for inhibiting
XX cellular proliferation, when administered with a p53 protein. The RTPSPs
XX can be used for treating diseases characterised by abnormal cellular
XX proliferation, particularly cancers. The RTPSPs have a broader spectrum of
XX activity than wild type RTPSPs.

SQ Sequence 3161 RP: 1837 A; 619 C; 586 G; 919 T; 0 other;

Alignment Scores:
Prod. No.: 0 Length: 3161
Score: 4144.00 Matches: 797
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

LS 09 120 459A-45 (1-797) x AAV58449 (1-3161)

QV : MetProGlyThrProArgLysThrAlaAlaAlaAlaAlaAlaAlaGluPro 20
DB: 1 ATGGCGCTTAAACATCCCTTGAAAAAGATTGTAATGTGTTATGGTAGGTAATAAT 56
QV : ProAlaIleProProProProProGluGluAspProGluClnAspSerGlyProGlu 40
DB: 1 CTGGCAAG 126
QV : AspLeuProLeuValArqLeuGlupheGluGluThrGluGluProAspPheThrAlaLeu 60
DB: 1 GTTCGCGCTTCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 186
QV : CysGlnLysLeuLysIleProAspHisValArqGluArqAlaTrpLeuThrTrpGluLys 80
DB: 1 TGTCACAAATTAAACATACCAGCATATGTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
QV : ValSerSerValAspGlyValLeuClyGlyTyrIleGlnLysLysLysGluLeuTrpGly 100
DB: 247 GTTTATATCTGATGAGTATTGACAGCTTATTATTAAGAAGAAAAGGAACCTGTGGGA 306
QV : IleCysIlePheIleAlaAlaValAspLeuAlaValIleProIleAsnGlySerProArq 120
DB: 1 ATCTGACTTCTTATTCACAGCTTGACCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 366
QV : TrpProArqArgClycylAsnArgSerAlaArtileAlalysGlnleuGluAsnAspThr 140
DB: 1 AAG 426
QV : ArgIleIleIleValIleuLysLysLysLysLysLysLysLysLysLysLysLysLys 160
DB: 1 AGAATATTTAGAGTCTCTGTGTANA-AAATATATCTAATATAATATATATATATATATAT 486

1387 GGCCTTAACTTAAAGCCCTTCATTTTACAAAGTGATCGAAAGCTTTTATCAAAAGCAGAA 1446
 400 GlyAsnLeuThrArgGlnMetIleLysHisLeuGluArgCysGluHisArgIleMetGlu 428
 1447 GGCACATTCACACAGACAAATGATGAAATTTAGAACCATGAGAACATCGCAATCATGCAA 1506
 420 SortouAlaTrpLeuSerAspSerProLeuPheAspIleuLysGlnSerLysAspArg 448
 1507 TCCCTTGATGGCTCCACATTCACCTTATTTGATCTTATTAACAAATCAAGAGACAGA 1566
 440 GlyGlyTrpThrAspHisGluSerAlaCysProLeuAsnIleuProLeuGlnAsnAsn 468
 1567 GACACGACACATCATCATCTTTCTCTCTCTTAACTTAACTTCTCTCTCTCTCTCTCTCT 1626
 460 HisThrAlaAlaAspMetTyrLeuSerProValArgSerPheCysLysLysGlySerThr 488
 1627 GACACGACACATCATCATCTTTCTCTCTCTTAACTTAACTTCTCTCTCTCTCTCTCTCT 1686
 480 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 508
 1687 AGGGTGTAATCTTACTGCAATATGACAGACATACAGCACTTACGCTTCTGAGACAG 1746
 500 LysTrpGluLysSerLysSerLeuLeuLeuLysLysValTyrArgGluAlaTyr 528
 1747 AAGCCATTCGAAATCATCT 1806
 520 LeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIle 548
 1807 GTCCGAGTAAATACACTTGTGAAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1866
 540 LeuTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHis 568
 1867 ATCTGAGCTTTTTCGAGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1926
 560 LeuAspGluIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 588
 1927 TTGACCAAAATATGATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1986
 580 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPhe 608
 1987 AAATTCGAAATCATCT 2046
 600 LysArgValLeuIleLysCysGluGluTyrAspSerIleIleValPheTyrAsnSerVal 628
 2047 AAACGTGTTTTCATCAAGAGAGAGATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2106
 620 PheMetGlnArgLeuLysThrAsnIleLeuGluTyrAlaSerThrAspTrpTrpIleLeu 648
 2107 TCAAGCAATACATCAAAACAAATATTTGATGATGCTCTCTCTCTCTCTCTCTCTCTCT 2166
 640 SerProIleProHisIleProArgSerProTyrLysPheProSerSerProLeuArgIle 668
 2167 TCAAGCAATACATCAAAACAAATATTTGATGATGCTCTCTCTCTCTCTCTCTCTCTCT 2226
 660 ProGlyTyrAsnIleThrSerIleLeuLysSerProTyrLysLysCysGluGluLeu 688
 2227 TCAAGCAATACATCAAAACAAATATTTGATGATGCTCTCTCTCTCTCTCTCTCTCTCT 2286
 680 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPhe 708
 2287 TCAAGCAATACATCAAAACAAATATTTGATGATGCTCTCTCTCTCTCTCTCTCTCTCT 2346
 700 GlyThrSerValLysPheGlnTyrIleAsnIleLeuValLysAsnSerAspArgValLeu 728
 2347 GGCACATTCGCAAGTTCGCAAGTTCGCAAGTTCGCAAGTTCGCAAGTTCGCAAGTTCG 2406
 720 LysArgSerAlaGluGlySerAsnProLysProLeuLysLysLysLysLysLysLys 748
 2407 AAAGAGAGTTCGCAAGTTCGCAAGTTCGCAAGTTCGCAAGTTCGCAAGTTCGCAAGTTC 2466
 740 GluGlySerAspSerAlaAspGlyLysHisLeuProGlyCysLysPheGlnGln 768

Db 2467 CAAGCATCATGACAGACAGATGCAAGTAAATAAATATCTCCAGCAGAGTCCAAATTTCCAGCAC 2526
 QY 769 LysLeuAlaGluMetThrSerThrArgMetGlyLysGlnLysMetAsnAspSer 788
 Db 2527 AAATCTGATGAAATATTTATCTGAAATATGAAATATGAAATATGAAATATGAAATATG 2586
 QY 789 MetAspThrSerAsnLysGluGluLys 797
 Db 2587 ATGGATACCTCAATCAAGAGAGAGAA 2613
 RESULT 4
 ID AAQ41545
 AC AAQ41545
 XX 24-AUG-1993 (first entry)
 DE Retinoblastoma gene.
 KW RR gene product; p56RB portion; cell cycle progression control;
 KW combination; therapeutic methods; arrest; tumorigenesis;
 KW regulation; physiological processes; blood cell product;
 KW gamete prodn.; ss.
 XX Homo sapiens SP-40 cell line.
 XX Key Location/Qualifiers
 FT CDS 139..2925
 FT /*tag= a
 FT /note= "Rb protein"
 XX W09308267-A.
 XX 29-APR-1993.
 XX 16-OCT-1992; 92MO-US08918.
 XX 17-MAR-1991; 91US-0778410.
 XX (REGC) UNIV CALIFORNIA.
 XX Goodrich DW, Lee EYHP, Lee WH, Wang NP;
 DR WPI; 1993-152462/18.
 DR P-PSDB; AAE36534.
 XX Method of controlling cell cycle progression uses purified
 retinoblastoma protein or fragment, for use in combination with
 therapeutic methods to arrest tumorigenesis
 XX Disclosure, Fig 9, 68pp, English.
 CC the sequence is that of the retinoblastoma gene which encodes the
 retinoblastoma (RB) protein which may be used as part of a method of
 controlling cell cycle progression which may be used in combination
 with therapeutic methods to arrest tumorigenesis in organisms. The
 cell cycle can be reversibly arrested in a convenient and safe
 manner. The protein is used in a compsn. is relatively inexpensive
 and readily obtainable, and shows little or no toxic effects on
 healthy cells. It is also compatible with other methods and devices
 for regulating certain physiological processes of the body, such as
 blood cell prodn. and gamete prodn. Fragments of the protein are
 soluble in low concns. of glycerol, thus enhancing their value in
 pharmaceutical applns.
 XX Sequence 2994 BP; 974 A; 618 C; 594 G; 808 T; 0 other;
 Alignment Scores:
 Pred No. 0 Length 2994
 Score: 4068.50 Matches 797
 Percent Similarity: 85.88% Conservatio. 0
 Best local Similarity: 85.88% Mismatches: 0


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1b 2179 TGGAGCTTTTTCACACACCTGTGACAAATGAGTATGAACCTCATGAGACACAGGATTTG 2248
QY 570 AspIndLeuMetMetCysSerMetTyrGlyTleCysLysValLysAsnLleAspLeuLys 589
1b 2249 GACAAATATATGATGCTTCTGACGATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2298
QY 590 PheLysLleLleValThrAlaTyrLysAspLeuProLisAlaValGlnGluThrPheLys 609
1b 2299 TTAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2358
QY 610 ArgValLleLleLysLleLysLleLysLleLysLleLysLleLysLleLysLleLysLle 629
1b 2359 GGTGTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2418
QY 630 MetGlnArgLysThrAspLleLysLleLysLleLysLleLysLleLysLleLysLleLys 649
1b 2419 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2478
QY 650 ProLysProLisLleProArgSerProTyrLysPheProSerSerProLeuArgLlePro 669
1b 2479 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2538
QY 670 GlyGlyAsnLleLysLleLysLleLysLleLysLleLysLleLysLleLysLleLysLle 689
1b 2539 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2598
QY 690 ThrProThrLysMetThrProArgSerArgLleLysValSerLleGlyLysSerPheGly 709
1b 2599 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2658
QY 710 ThrSerGlnLysPheGlnLysLleAsnLleMetValCysAspSerAspArgValLleLys 729
1b 2659 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2718
QY 730 ArgSerAlaGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 749
1b 2719 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2778
QY 750 CysSerAspGlnAlaAspLysLysLysLysLysLysLysLysLysLysLysLysLysLys 769
1b 2779 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2838
QY 770 LeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAspSerMet 789
1b 2839 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2898
QY 790 AspLysSerAsnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 797
1b 2899 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2922
RESULT 9
AA004474
1b AA004474 standard: cDNA: 2995 bp.
XX AA004474:
XX
XX 04 JUN 2003 (first entry)
XX
XX Retinoblastoma tumour suppressor protein, p10RB cDNA.
XX
XX Retinoblastoma: RB tumour suppressor protein; p10RB; p53; gene therapy;
XX cystic fibrosis; and thyroid, and pituitary, adenoviral protein IX; psoriasis;
XX thyroid hyperplasia; Graves disease; hepatocellular carcinoma; neoplasms;
XX benign prostatic hypertrophy; Li-Fraumeni syndrome; sickle cell anemia;
XX Tay Sachs disease; leukemias; lymphoma; adenovirus vector; cancer; ss.
XX unidentified.
XX
XX K07 location/qualifiers
XX CUS /product
XX /product
XX p10RB*

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XX
PN US6210949-B1.
XX
PD 03-APR-2001.
XX
XX 25-OCT-1994: 940S-0128673.
XX
XX 25-OCT-1994: 940S-0142669.
XX
XX 19-MAY-1994: 940S-0233777.
XX
XX (CANU-) CANU1 INC.
XX
XX Gregory RJ, Wells KN, Maneval DC.
XX
XX WPI: 2001-289633/30.
XX
XX P-PSDB: AAE00689.
XX
XX New recombinant adenovirus expression vector having a gene encoding for
XX a foreign protein and a partial or total deletion of the adenoviral
XX protein IX DNA, useful in gene therapy for treating or reducing
XX hyperproliferative cells.
XX
XX Disclosure: Fig 3; 49pp; English.
XX
XX The present cDNA sequence encodes retinoblastoma (RB) tumour suppressor
XX protein, designated as p10RB.
XX
XX The invention relates to a recombinant adenovirus expression vector
XX characterised by the partial or total deletion of the adenoviral protein
XX IX DNA beginning at nucleotides 457 or 360 and ending at 4920 4050, and
XX having a gene encoding a foreign protein such as tumour suppressor
XX protein, p10RB (retinoblastoma) and p53. Adenovirus vector is used
XX for screening tumour suppressor genes useful in gene therapy. The vector
XX is particularly useful for treating or reducing hyperproliferative cell
XX disorders such as thyroid hyperplasia, Grave's disease, psoriasis,
XX benign prostatic hypertrophy, Li-Fraumeni syndrome, leukemias, etc. to
XX inhibit tumour proliferation or to ameliorate particular related
XX pathology such as sickle cell anaemia and Tay-Sachs disease, the vector
XX is also useful for the safe recombinant production of diagnostic and
XX therapeutic polypeptides and proteins.
XX
XX Sequence 2995 BP: 975 A; 618 G; 594 C; 809 T; 0 other.
SQ

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Alignment Scores:
Pred. No.: 0 Length: 2995
Score: 4068.50 Matches: 797
Percent Similarity: 85.88% CrossMatches: 0
Best Local Similarity: 85.88% Mismatches: 0
Query Match: 98.18% Indels: 141
DB: 22 Gaps: 1

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US-09-026 459A-45 (1-797) x AAD04474 (1-2995)

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QY 1 MetProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAlaAlaPro 20
DB 139 ATGCGCGCCAAACCCCGCGGAAACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 198
QY 21 ProAlaProLysProLysProLysProLysProLysProLysProLysProLysProLys 40
DB 199 GAGGACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 258
QY 41 AspLeuProLeuValArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeu 60
DB 259 GACTGGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 418
QY 61 CysGlnLysLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 80
DB 419 TGTCAAAATTAAGATACAGATCATGTGACAGACAGAGTTGGTTAAATTTCAGAGAAA 478
QY 81 ValSerSerValAspGlyValLleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 479 GTTTCATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 498

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Pred. No.: 0                      Length: 4555
Score: 4068.50                    Matches: 797
Percent Similarity: 85.88%        Conserved: 0
Best Local Similarity: 85.88%     Mismatches: 0
Query Match: 98.18%              Indels: 141
db: 19                            Gaps: 1

US 09 026 459A 4% (1-797) x AAV6H440 (1-4555)

Q7 1 MetProProLysThrProAlaGlyThrAlaAlaThrAlaAlaAlaAlaAlaGluPro 20
db 1 ATGCGGCAAAACCGCGGCAAAACCGCGGCAAAACCGCGGCAAAACCGCGGCAAAACCG 66
Q7 21 ProAlaProProProProProProGluGluAspProGluGluAspSerGlyProGlu 40
db 67 GAGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 126
Q7 41 AspLeuProLeuValAlaLeuGluGluGluGluGluGluGluGluGluGluGluGlu 60
db 127 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 186
Q7 61 CysGlnLysLeuLysThrProAspHisValAlaAlaAlaAlaAlaAlaAlaAlaAla 80
db 187 TGTAGAAATTAAGGATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 246
Q7 81 ValSerSerValAspGlyValLeuGlyGlyTyrIleGlyGlyLysLysGluLeuTrpGly 100
db 247 GGTGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 306
Q7 101 IleCysIlePheIleAlaAlaValAspLeu----- 110
db 407 ATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 366
Q7 110 ----- 110
db 467 CAGAAAGCATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 426
Q7 110 ----- 110
db 427 AGTAAAGGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
Q7 110 ----- 110
db 487 CTCTTTAGGAAATTTGGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
Q7 110 ----- 110
db 947 ATATCTATTAATAAATTTGCGATTGGTGTAAAGATTTCTTGGATGATGATTTATTA 606
Q7 110 ----- 110
db 607 GATAAAGGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666
Q7 110 ----- 110
db 667 TGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 726
Q7 111 AlaValIleProIleAsnGlySerProAlaAlaProAlaAlaAlaAlaAlaAlaAla 129
db 727 ACAGCTGTTATAGCGGATTAAGGCTTCAGCTGCAAGGAGGAGGAGGAGGAGGAGGAG 786
Q7 140 AlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 149
db 787 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
Q7 160 HisGlyLysAsnIleAspGluValLysAsnValTyrPheLysAsnIleProPheMet 169
db 847 CATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 906
Q7 170 AsnSerIleGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArg 189
db 907 AATTCCTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGG 966

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QY 190 TyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaAlaAlaAlaAlaAlaAla 209
db 967 TACCAAGCAAAATTAATCTTAAATAAAGACCTAGACAGCAAAATTAATCTTAAATAA 1026
QY 210 LysThrLeuGluThrAspSerIleAspSerPheGluThrGluAlaAlaAlaAlaAla 229
db 1027 AAAACCTCTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1086
QY 240 AsnLeuAspGluGluValAsnValIleProProHisIleProValAlaAlaAlaAla 249
db 1087 AACCTTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1146
QY 250 ThrIleGlnIleLeuMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 269
db 1147 ACTATCCAAATAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1206
QY 270 IleSerThrPheAsnAspCysThrValAspProGlySerIleLeuLysAlaAlaLys 289
db 1207 ATTTCTCTATTTAACAACTGACAGTCAATGCAAAAGAAAGTATATGAAAGAAAGTGA 1266
QY 290 AspIleGlyTyrIleCysGlyGluLysPheAlaLysAlaValGlyGlyGlyValGlu 309
db 1267 GATATAGCAATCAATCTTAAAGACAAATTTGCTAAAGCTGAGAACTGAGTAAATG 1326
QY 310 IleGlySerGlnArgTyrLysLeuGlyValAlaAlaLysTyrTyrArgValIleGluSerMet 429
db 1327 ATTGGATCAGAGGATACAAACTTGGAGTTGGTTCGTTATATGAGTAAATGCAATG 1386
QY 330 LeuLysSerGluGluGluAlaAlaLeuSerIleGlnAspPheSerLysLeuLeuAsnAsp 349
db 1387 CTTAAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1446
QY 350 IlePheHisMetSerLeuLeuAlaCysAlaLeuGluValAlaIleMetAlaIleTyrSerArg 369
db 1447 ATTTTCATATGCTTTATTTGGCTGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT 1506
QY 370 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnVal 389
db 1507 AGTACATCTCAGAACTGATGATGAGAACTGATGATGATGATGATGATGATGATGATG 1566
QY 390 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaIleLys 409
db 1567 CTTAAATTTAAAGCTTTGATTTTAAAGCTGATGAGAGCTTATCAAACTTCAAACT 1626
QY 410 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisSaraIleMetGluSer 429
db 1627 AACCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1686
QY 440 LeuAlaIleAsnSerAspSerPheAspLeuIleLysLeuSerLysAspAlaGlu 449
db 1687 CTTCGATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1746
QY 450 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGluAsnAspHis 469
db 1747 GGAGCAACTATCACTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1806
QY 470 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysLysLysThr 489
db 1807 ACTGACACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1866
QY 490 ArgValIleAsnSerThrAlaAsnAlaGluThrGluAlaAlaAlaAlaAlaAlaAla 509
db 1867 CGTGTAATTTCTACTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1926
QY 510 ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeu 529
db 1927 GCATTGAAATCTATGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1986
QY 540 ArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProLeuLeuGluHisIleLeu 549
db 1987 CGGCTAAATACACTTTGCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2046
QY 550 TrpThrLeuPheGlnIleHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAlaHisLeu 569

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47 110 ----- 110
4b 427 AGTAACTAAGGATGAAATGTAAGTCAAGAGAGTCTTCAAGACAGATATGATGATTTGCGCA 486
47 110 ----- 110
4b 487 CTCTTCAAGAAATGGAAGAAAGAAATGAGAAATTAATAATTAATGAAATGAAATGAAATG 546
47 110 ----- 110
4b 547 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 606
47 110 ----- 110
4b 607 GTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 666
47 110 ----- 110
4b 667 TGTGCTTGAATATTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
47 111 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 729
4b 727 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
47 130 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 149
4b 787 GTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 846
47 150 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 169
4b 847 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
47 170 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 189
4b 907 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
47 190 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 209
4b 967 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
47 210 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 229
4b 1027 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
47 230 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 249
4b 1087 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
47 250 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269
4b 1147 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
47 270 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 289
4b 1207 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1266
47 290 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 309
4b 1267 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
47 310 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 329
4b 1327 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
47 330 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 349
4b 1387 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
47 350 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 369
4b 1447 AATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506

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470 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProIleIleLeuAsnVal 489
4b 1507 AGTAACTAAGGATGAAATGTAAGTCAAGAGAGTCTTCAAGACAGATATGATGATTTGCGCA 1566
47 390 LeuAsnLeuLysAlaPheAspPheLysValIleGluSerPheIleLysAlaGluIle 409
4b 1567 CTAAATTTAAAGGCTTTGATTTTAAAGAGATGAGGAAAGTTTATCAAAAGAAAGAAAG 1626
47 410 AsnLeuThrArgIleMetIleLysHisLeuGluAsnLysLeuLysLeuLysLeuLysLeu 429
4b 1627 AACTTCAACACACAAAGATTAAGAAATTAAGACCAAGTGAATATGCTTCTTAAATCTTCT 1686
47 430 LeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysLeuSerLysAspArgIle 449
4b 1687 CTTCAGAGGCTCTCAAGATTAAGCTTAAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 1746
47 450 GlyProThrAspHisLeuGluSerAlaLysProLeuAsnLeuProLeuGlnAsnAsnHis 469
4b 1747 GGACCAACTGATCAGCTTGAATCTGCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCTT 1806
47 470 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysLysLysLys 489
4b 1807 ACTGCCACACATATGTAATCTTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCTTCT 1866
47 490 ArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAlaPheGluThrGluLys 509
4b 1867 CGCTAAATCTTCTTAAATCTTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCTTCT 1926
47 510 ProLeuLysSerThrSerLeuSerLeuPheLysLysLysLysLysLysLysLysLys 529
4b 1927 CATTGAAATCTTCTTAAATCTTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCTTCT 1986
47 530 ArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProLeuGluGluHisIleIle 549
4b 1987 CGGTAAATACACTTCTTCAAGAGGCTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCT 2046
47 550 TrpThrLeuPheGluHisThrLeuGluAsnGluTyrGluLeuMetArgAspArgHisLeu 569
4b 2047 TGGACCTCTTCTTCAAGAGGCTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCTTCT 2106
47 570 AspLeuIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnLeuAspLeuLys 589
4b 2107 GACCAATTTATGATCTTCTTCAAGAGGCTCTTGTCTTAAATCTTCTTAAATCTTCTTAA 2166
47 590 PheLysIleIleValThrAlaLysLysAspLeuPheHisAlaValGluGluThrPheLys 609
4b 2167 TTTCAAAATCTTCTTCAAGAGGCTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCTTCT 2226
47 610 ArgValLeuIleLysGluGluTyrAspSerIleIleValPheTyrAsnSerValPhe 629
4b 2227 CGCTTCTTCAAGAGGCTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCTTCTTAAATCT 2286
47 630 MetGlnArgLeuLysThrAsnIleLeuGluTyrAlaSerThrArgProThrLeuSer 649
4b 2287 ATGCAAGAGTGAATAATTTTCAAGAGGCTCTTGTCTTAAATCTTCTTAAATCTTCTTAA 2346
47 650 ProIlePheHisIleProArgSerProLysPheProSerSerProLeuArgIlePro 669
4b 2347 CCAATACCTGATCTTCTTCAAGAGGCTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCT 2406
47 670 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerIleGluLeuPro 689
4b 2407 GGACGGCAATCTTATATTTCAAGAGGCTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCT 2466
47 690 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyLysSerPheLys 709
4b 2467 ACACCAAAATGATCTTCAAGAGGCTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCTTCT 2526
47 710 ThrSerGluLysPheGluLysIleAsnGluMetValPheLysAsnSerAspArgValLeuLys 729
4b 2527 ACTTCTGAGAGTCTTCAAGAGGCTCTTGTCTTAAATCTTCTTAAATCTTCTTAAATCTTCT 2586
47 740 ArgSerAlaGluLysSerAsnProLysProLeuLysLysLysLysLysLysLysLysLys 749

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10 1518 CTTAAATACAAACAAACAAATATATATCAAAATTTTACGAAATCTCTGAAAGACAAAC 1577
27 450 TTTTPhelHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 369
10 1578 ATTTTTCATAGCTTTTATTGAGTGCGGCTCTTGAAGTTGTAAATGCCACATATAGCAGA 1637
27 470 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProThrIleLeuAsnVal 389
10 1648 AGTAAATCTGAGATCTGATTTGGAAAGAGATTGTCTTTGGCATGGATTCTGAATGTG 1697
27 490 LeuAsnLeuLysAlaPheAspPheTyrLeuValIleLeuAspSerPheIleLysAlaGluCly 409
10 1698 CTTAAATTTAAAGGCTTTTCAATTTTACAAGTCATGAAAGTTTATCAAGACCAAGAGC 1757
27 410 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSer 429
10 1758 AATTTTGAAGCAAAATGATATAAATATTTGAAGAGATGTCATATGAAATCATAGGAATTC 1817
27 440 LeuAlaThrLeuSerAspSerProLeuPheAspGluLeuLysSerThrAspArgGlu 449
10 1818 CTTTCAATGAGCTCAATATGAGTTTATTATTGATCTTATTAAATCAATCAAGAGCGAGAA 1877
27 450 GlyProThrAspIleLeuAlaCysPheLeuAsnLeuProLeuGluAlaAsnAspHis 469
10 1878 GGAACAAATGATCACTTGAATATGCTTGGTCCCTGCTTAAATCTGCTGCTGCTGCTGCTG 1937
27 470 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysLysSerThrThr 489
10 1938 AATTCATATATATATATCTTTCTCTGTAGATCTCTCAAGAGAGAGAGAGAGAGAGAGAG 1997
27 490 ArgValAsnSerThrAlaAlaGluThrGlnAlaThrSerAlaPheGlnIleIleGlnHis 509
10 1998 GGTGTAATATTTATGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2057
27 510 ProLeuLysSerThrSerLeuSerLeuPheSerTyrLysLysValTyrArgLeuAlaTyrLeu 529
10 2058 CCAATCAAAATCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2117
27 540 ArgLeuAsnThrLeuCysIleArgLeuLeuSerGluHisProGluLeuGluHisIleIle 549
10 2118 CAGTAAATATATGATTTGTAAGAGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2177
27 560 TrpIleLeuPheThrIleHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 569
10 2178 TGAAATTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2237
27 570 AspIleIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 589
10 2238 GAAACAAATATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2297
27 590 PheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGluGluThrPheLys 609
10 2298 TTTAAATATCTTAAAGAGATATGAGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2357
27 610 ArgValLeuIleLysGluGluThrAspSerIleIleValPheLysAsnSerValPhe 629
10 2358 GGTGTTTTCAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2417
27 640 MetGluArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSer 649
10 2418 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2477
27 660 ProIleProHisIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 669
10 2478 CCAATATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCT 2537
27 670 GlyLysAsnIleThrSerProLeuLysSerProLysIleSerGluLysLeuPro 689
10 2538 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2597
27 690 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyLysSerPheGly 709
10 2598 AATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAAT 2657

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27 710 ThrSerGluLysPheGlnLysIleAsnGluMetValTyrAsnSerAspArgIleLys 729
10 2658 ACTTCTGAGAGAGTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2717
27 730 ArgSerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGlu 749
10 2718 AGAAGTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2777
27 750 GlySerAspGluAlaAspGlySerLysHisLeuProGlyLysSerLysPheGlnLys 769
10 2778 GGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2837
27 770 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysLysLysMetAsnAspSerMet 789
10 2838 CTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2897
27 790 AspThrSerAsnLysGluGluLys 797
10 2898 GATACCTCAAAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2957

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Search completed: January 18, 2003, 08:49:13
Job time : 359.994 secs

Genware version 5.1.1.3
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CM nucleic nucleic search, using SW model

Run on: January 16, 2003, 15:20:17 : Search time 433.783 Seconds
(without alignments)
17541.794 Million cell updates/sec

Title: US 09-026-459A 46
Perfect score: 4377
Sequence: 1 CCGGCAAGCGGCAAAAC.....AAATCAGATTATTCATAGT 3377

Scoring table:
IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1155999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:	N	Geneset	HitID	Score	Match	Length	DB ID	Description
1:	1	US09026459A	4377	100.0	4377	19	AAV58450	Modified retinobla
2:	2	US09026459A	3555	94.3	3555	19	AAV58440	Modified retinobla
3:	3	US09026459A	3556	94.3	3556	19	AAV58440	DNA sequence of th
4:	4	US09026459A	4849	94.2	4849	21	AAA29491	Human retinoblasto
5:	5	US09026459A	4849	94.2	4849	21	AAZ88444	Human androgen rec
6:	6	US09026459A	4849	94.2	4849	24	ABL26283	Breast cancer rela
7:	7	US09026459A	4849	94.2	4849	24	AAV58452	Modified retinobla
8:	8	US09026459A	4849	94.2	4849	19	AAV58451	Modified retinobla
9:	9	US09026459A	4849	94.2	4849	15	AAU70536	Human retinoblasto

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	4377	100.0	4377	19	AAV58450
2	3184.6	94.3	3555	19	AAV58440
3	3184.6	94.3	3556	19	AAV58440
4	3182.6	94.2	4849	21	AAA29491
5	3182.6	94.2	4849	21	AAZ88444
6	3182.6	94.2	4849	24	ABL26283
7	3180.4	94.2	4849	24	AAV58452
8	3169	94.6	4849	19	AAV58451
9	3153	94.4	4597	15	AAU70536

10	3153	93.4	4597	20	AAU04501
11	3151.4	93.3	4597	5	AAH81369
12	3148.4	93.2	4740	24	ABK86579
13	3111	92.1	3347	19	AAV58448
14	3094	91.6	4579	9	AAH81261
15	3076.6	91.1	3455	19	AAV58441
16	3012.6	89.2	3392	19	AAV58442
17	2984.4	88.4	3461	19	AAV58447
18	2944.6	87.2	3423	19	AAV58443
19	2945	86.9	3161	19	AAV58449
20	2886.6	85.5	3266	19	AAV58444
21	2855.6	84.6	3323	19	AAV58446
22	2841.6	84.1	3218	19	AAV58491
23	2841	84.1	3213	15	AAU72690
24	2825	83.7	3113	19	AAV58445
25	2766.6	81.9	5056	10	AAH90489
26	2490.6	73.8	2994	19	AAV40004
27	2489	73.7	2994	14	AAU41545
28	2489	73.7	2994	21	AAU43287
29	2487.6	73.7	2995	20	AAH90450
30	2487.6	73.7	2995	22	AAH25955
31	2487.6	73.7	2995	22	AAU04474
32	2487.6	73.7	2995	23	ABL59404
33	2487.4	73.7	2994	11	AAU04713
34	2486	73.6	2995	16	AAU00959
35	2486	73.6	2995	16	AAU086398
36	2484.4	73.6	2995	20	AAU00737
37	835	24.7	18303	20	AAU04562
38	831.8	24.6	18177	10	AAH90490
39	220.8	6.5	1698	18	AAU62396
40	220.8	6.5	1802	18	AAU62391
41	220.8	6.5	1802	18	AAU62391
42	220.8	6.5	1802	18	AAU62391
43	220.8	6.5	1802	18	AAU62391
44	218.8	6.5	1697	15	AAU01542
45	218.8	6.5	1697	15	AAU01541

ALIGNMENTS

RESULT 1

AAV58450 standard; DNA; 3377 bp.

AAV58450:

02-DEC-1998 (first entry)

Modified retinoblastoma tumor suppressor gene.

Modified retinoblastoma tumor suppressor gene, RBP protein, cancer therapy;
cellular proliferation inhibitor; 38.

Homo sapiens.

Key Location/Qualifiers

FT CDS /tag - a

W09847091-A2.

27-AUG-1998.

19-FEB-1998; 98W0-0503041.

20-FEB-1997; 97US-0038118.

(DAYU) BAYLOR COLLEGE MEDICINE.

(TEXA) UNIV TEXAS SYSTEM.

Benedict WF, Hu S, Xu H, Zhou Y;

QY 1864 ATCACTGAGGAGGCTTTGGCAATACATGCTGAGAAAGAGATATGAACATCAAGAGACAGG 1923
 DB 2041 ATCACTGAGGAGGCTTTGGCAATACATGCTGAGAAAGAGATATGAACATCAAGAGACAGG 2100
 QY 1924 CATTTGGCAATCAATCAAG 1983
 DB 2101 CATTTGGCAATCAATCAAG 2160
 QY 1984 CTAAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2043
 DB 2161 CTAAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
 QY 2044 TTTAAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2103
 DB 2221 TTTAAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
 QY 2104 GTTCAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2163
 DB 2281 GTTCAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
 QY 2164 TTTAAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2223
 DB 2341 TTTAAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
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 DB 2401 ATTTTAAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
 QY 2284 GTTCAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2343
 DB 2461 GTTCAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
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 DB 2821 GTTCAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
 QY 2704 TTTAAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2763
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 DB 3001 ATTTTAAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060
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 DB 3061 ATTTTAAATTCAGAAATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120

QY 2944 CTTCTGCTGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3003
 DB 3121 CTTCTGCTGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
 QY 3004 TAAATTTATATGATATATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 3063
 DB 3181 TAAATTTATATGATATATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 3240
 QY 3064 ATCTTCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3123
 DB 3241 ATCTTCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3300
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 QY 3184 TTACTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3243
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 DB 3481 CCTCAGAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 3540
 QY 3364 GGATTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3423
 DB 3541 GGATTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3600

RESULT 3

AAV54990

ID AAV54990 standard; DNA; 3555 BP.

AC AAV54990;

ET 26-NOV-1998 (first entry)

XX DNA sequence of the specification.

XX Minimal promoter, tetracycline responsive expression vector; IRV;

XX transcriptional transactivation domain; TTD;

XX tetracycline repressor protein; TRP; tetracycline operator;

XX production; stable cell line; protein production;

XX tumour suppressor protein; treatment; cancer; ss.

XX Unidentified.

XX Key Location/Qualifiers

FH CDS 7...2794

FT /*tag- a

XX WO9837185-A2.

XX 27-AUG-1998.

XX 19-FEB-1998; 98WO-US03092.

XX 20-FEB-1997; 97US-0048755.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Hu S, Logothetis CJ, Xu H, Zhou Y;

XX WPI; 1998-480796/41.

XX P-PSDB; AAW71354.

New tetracycline responsive expression vectors - used for the
 tightly controlled expression of genes, such as tumour suppressor
 genes for treating cancers

XX WF: 2000-40055/34.

XX

XX New method for increasing the proliferative capacity of cell lines

PT comprises administering agents reversibly activating telomerase

PI activity and reversibly inactivating Rb/p16INK4 and/or p53 pathways useful

PI in treating age related diseases

XX

XX claim 5: Para 121-123; 123pp: English.

XX

XX The invention concerns methods and reagents for extending the life-span,

CC e.g. the number of mitotic divisions, of a cell. The method relies on

CC activation of a telomerase activity and inhibition of one or both of a

CC retinoblastoma (Rb)/p16INK4 pathway or a p53 pathway. Phosphorylation of Rb

CC by cyclin dependent kinases, cdk4 and cdk6, releases the cells into the

CC division cycle. Binding of INK4 family members, e.g. the tumour

CC suppressor p16INK4a, inhibits kinase activity and results in growth

CC arrest. Rb inactivators can selectively and reversibly inactivate an

CC p16INK4 pathway, especially at Rb/p16INK4 pathway. The anti-protein MDM2

CC is a cellular inhibitor of Rb/p21 function and the p53 tumour suppressor

CC and can also be used in the methods. Other molecules which can be used

CC include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which

CC differs from at one or more of residues K22, F34, H45 and L74.

CC Additional constructs include a papilloma virus E7 protein, or other

CC viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of

CC the Rb and p16INK4 genes may also be used. The methods are useful for

CC increasing the proliferative capacity of cells. The cells are

CC subsequently of use in pharmaceutical and cosmetic preparations used to

CC treat conditions related to (premature) ageing, e.g. muscular degeneration

CC and arteriosclerosis. The cells can also be used to replace tumour cell

CC lines in vitro and for studies on biochemical and physiological aspects

CC of growth and differentiation. Long lived (immortal) cells could also be

CC of use in the production of normal or genetically engineered

CC biotechnology products.

XX

XX Sequence 4839 BP; 1534 A; 902 C; 880 G; 1523 T; 0 other;

XX

XX Query Match 94.2% Score 3182.6 DB 2L Length 4839;

XX Best Local Similarity 94.9% Pred No 0;

XX Matches 3372; Conservative 0; Mismatches 4; Indels 177; Gaps 1

XX

XX 2 GGAGCAGCGGCTTAAATTTTTTTTCAAAAATGGTGTTCATTGCTGGTCTTGCTGGTGGCGG 61

XX 3111

XX 133 AGGCATCATGCCAACACCCCACAAAAAGCGGGCACGTCGCGCGCGCGCGCGCGCGCG 192

XX

XX 62 AACGCGCGGTAATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 121

XX 193 AACGCGCGGTAATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 252

XX

XX 124 CGTAAATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTG 181

XX 253 CGTAAATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTG 312

XX

XX 182 CATATGTCACAAATAAAGAATCCAGATCATGTCAGACAGACAGCTGCTTAACATGGG 241

XX 313 CATATGTCACAAATAAAGAATCATGTCAGACAGACAGCTGCTTAACATGGG 372

XX

XX 242 ATAAATTTTCATGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCTGCTG 301

XX 473 ATAAATTTTCATGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCTGCTG 432

XX

XX 462 GGGTAATGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCTGCTGCTGCTG 361

XX 433 GGGTAATGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCTGCTGCTGCTG 462

XX

XX 462 AGTATCAAAAAACAAGAAATCAGTGGCCATAAATCTTAACTACTAAAAACAATG 421

XX 193 ACTATCAAAAAACAAGAAATCAGTGGCCATAAATCTTAACTACTAAAAACAATG 552

XX

XX 422 ATATCAATACCAAATCTGATGAATGCTATGTCAGAGACTGTTGAAGAGCTATGATGCTAT 481

XX 533 ATATCAATACCAAATCTGATGAATGCTATGTCAGAGACTGTTGAAGAGCTATGATGCTAT 612

1693 ATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAAGTTTATCAAAAGCAG 1752
1445 AAGGCAAAATTCAGCAAGCAAAACAAATTAAGAAATGATGCAAAATGATGCAAAATGATG 1504
1753 AAGGCAAAATTCAGCAAGCAAAACAAATTAAGAAATGATGCAAAATGATGCAAAATGATG 1812
1505 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 1564
1813 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 1872
1565 GAGAAAGCAAAATTCAGCAAGCAAAACAAATTAAGAAATGATGCAAAATGATGCAAAATGATG 1624
1873 GAGAAAGCAAAATTCAGCAAGCAAAACAAATTAAGAAATGATGCAAAATGATGCAAAATGATG 1932
1625 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 1684
1933 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 1992
1685 GAGAAAGCAAAATTCAGCAAGCAAAACAAATTAAGAAATGATGCAAAATGATGCAAAATGATG 1744
1993 GAGAAAGCAAAATTCAGCAAGCAAAACAAATTAAGAAATGATGCAAAATGATGCAAAATGATG 2052
1745 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 1804
2053 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2112
1805 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 1864
2113 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2172
1865 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 1924
2173 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2232
1925 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 1984
2233 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2292
1985 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2044
2293 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2352
2045 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2104
2353 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2412
2105 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2164
2413 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2472
2165 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2224
2473 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2532
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2713 AATGCTGTTAAATTTAAAGAGTTGATTTTATCAAAATGATGCAAAATGATGCAAAATGATG 2772
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Db 2773 TTGAAGCATATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 2832
Qy 2525 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 2584
Db 2833 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 2892
Qy 2585 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 2644
Db 2893 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 2952
Qy 2645 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 2704
Db 2953 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3012
Qy 2705 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 2764
Db 3013 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3072
Qy 2765 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 2824
Db 3073 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3132
Qy 2825 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 2884
Db 3133 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3192
Qy 2885 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 2944
Db 3193 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3252
Qy 2945 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3004
Db 3253 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3312
Qy 3005 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3064
Db 3313 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3124
Qy 3065 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3124
Db 3373 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3184
Qy 3125 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3184
Db 3433 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3192
Qy 3185 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3244
Db 3493 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3302
Qy 3245 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3304
Db 3553 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3362
Qy 3305 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3364
Db 3613 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3422
Qy 3365 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3424
Db 3673 AGAAATGAGCAAAATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAAATTAATGAG 3482

REP01.1 5
AAZ88444
ID AAZ88444 standard; cDNA: 4839 BP.
XX
AC AAZ88444:
XX
DI 09-MAY-2000 (first entry)
XX
DE Human androgen receptor coactivator Rb encoding cDNA SEQ ID NO:7.
XX


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2815 AGATGAAAAATCTTGGTAAATGCTGCAATTTAAAAAGTGTGACAGCATTTTTCCTCT 2874
2821 AGATTGAAAAATCTTGTGTAATCTGCAATTTAAAAAGTGTGACAGCATTTTTCCTCT 2880
2875 TAAAGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2934
2881 TCAAGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
2945 TACCCAGGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2994
2941 TACCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
2995 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3054
3001 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
3055 GTCCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3114
3061 GTCCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
3115 GTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3174
3121 GTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
3175 GATTTTATTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3234
3181 GATTTTATTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
3245 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3294
3251 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3300
3295 GATTTTATTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3354
3301 GATTTTATTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
3365 TTTAAATGAGATTAATGATAGT 3377
3371 TTTAAATGAGATTAATGATAGT 3383

```

PSI 1.0
AA 70.66

XX AA 70.546 standard; DNA; 4597 BP.

XX AA 70.546;

XX 22 MAR 1995 (first entry)

XX Human retinoblastoma gene.

XX Retinoblastoma: cancer; detection; diagnosis; protein; neoplasm.

XX assay; immune complex; ss.

XX homo sapiens.

XX Key Location/Qualifiers

XX POS 347..2787

XX F1 /*tag= a

XX F1 80.4-A.

XX 27 JUL 1994.

XX 11 AUG 1987; 87bp-0307095.

XX 11 AUG 1986; 8605 0895163.

XX (MASS.) MASSACHUSETTS EYE & EAR INFIRMARY.

XX (WHED.) WHITEHEAD INST BIOMEDICAL RES.

XX 03/03/97; Friend S;

XX WHED 1994: 070246/24.
XX P-PSDR; AAF58568.
XX Diagnosing the presence of defective retinoblastoma alleles -
XX comprises comparing genetic material corresponding to a normal
XX human retinoblastoma with DNA from a patient.
XX Example 2(2); Figure 7; 18pp; English.
XX A method for detecting the presence, in a tumour sample, of a protein
XX the absence of which is associated with a neoplasm, comprises
XX producing an antibody to the protein and then contacting the
XX antibody with the tumour sample. Immune complexes indicate the
XX presence of the protein in the sample. The method may be used in
XX the detection and treatment of a defective human gene related to
XX cancer, in particular retinoblastoma.

XX Sequence 4597 BP; 1489 A; 841 C; 812 G; 1455 T; 0 other;

Query Match 93.4%; Score 3153; DB 15; Length 4597;

Best Local Similarity 94.8%; Pred. No. 0;

Matches 3366; Conservative 0; Mismatches 5; Indels 180; Gaps 4;

```

QY 4 GTCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63
DB 1 GTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 64 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 123
DB 61 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 118
QY 124 GAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
DB 119 GAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 177
QY 184 TTAGTCGACAAATTAATGATAGTATGATGATGATGATGATGATGATGATGAT 243
DB 178 TTAGTCGACAAATTAATGATAGTATGATGATGATGATGATGATGATGATGAT 237
QY 244 AAGTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
DB 238 AAGTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
QY 304 GGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
DB 298 GGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
QY 364 CTACACAAAAATACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
DB 358 CTACACAAAAATACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
QY 424 AGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
DB 418 ACACAGAACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 477
QY 484 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
DB 478 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
QY 544 TCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
DB 538 TCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 597
QY 549 ----- 548
DB 598 TTAGCTTAAAGGGGCAAGTATTACAAATGGAAGATGATCTGGTCAITTCATTCAGTAAATG 657
QY 549 ----- 548
DB 658 CTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
QY 549 --GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606

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[illegible]

D	b	1679	AGATTCACCTTTATTGATCTTTATTTAAAATAATCAAAAGAGATGAGAAAGATCAATATGATCA	17494
Q	y	1584	CCCTTGATCGCTGCTGCTGCTTAACTCTGCTCCACAGAAATATACATATGCTGACATAT	16443
D	b	1739	CCCTTGAATCGCTGCTGCTGCTTAACTCTGCTCCACAGAAATATACATATGCTGACATAT	17948
Q	y	1644	GTATCTTCTGCTGTAGATCTGCAAAANAAAAAGTTCACTACGCTGCTGTAAATTTATC	17043
D	b	1799	GTATCTTCTGCTGTAGATCTGCAAAANAAAAAGTTCACTACGCTGCTGTAAATTTATC	1858
Q	y	1704	TGCAAAATGACAGACACCAAGCAACCTTCAGCTTCAGAGCTCAGAGCTCATGCAAAATATC	17643
D	b	1859	TGCAAAATGACAGACACCAAGCAACCTTCAGCTTCAGAGCTCAGAGCTCATGCAAAATATC	1918
Q	y	1764	CTCTCTTTCACCTCTTTTATAAAAAAGTGTATCGGTAGCTATCTCGGCTTAAATATATCT	18243
D	b	1919	CTCTCTTTCACCTCTTTTATAAAAAAGTGTATCGGTAGCTATCTCGGCTTAAATATATCT	1978
Q	y	1824	TTGTGAAAGGCTTCTGCTGACAGACCAAAATTAAGATATATCATCTGAGCTTTTCTCA	1884
D	b	1974	TTGTGAAAGGCTTCTGCTGACAGACCAAAATTAAGATATATCATCTGAGCTTTTCTCA	2048
Q	y	1884	GCACACCTTCAGAAATACAGATCAACATCAAGACACAGCATTTGGACAAATATATCAT	19443
D	b	2049	GCACACCTTCAGAAATACAGATCAACATCAAGACACAGCATTTGGACAAATATATCAT	2098
Q	y	1944	CTCTTTCATCTATGCTATATATCAAAAGTCAAGCAATATACAGCTTAAATTTCAATTTCT	2003
D	b	2094	CTCTTTCATCTATGCTATATATCAAAAGTCAAGCAATATACAGCTTAAATTTCAATTTCT	2158
Q	y	2004	AACAGCATATACAGATCTCTCTATGCTGTACAGAAATATCAAAAGCTTTTGATCA	20643
D	b	2159	AACAGCATATACAGATCTCTCTATGCTGTACAGAAATATCAAAAGCTTTTGATCA	2218
Q	y	2064	AGAAGAGAGTATGATTTCTATTTATAGTATTAACCTCGCTTCTCAAGACATCA	2123
D	b	2219	AGAAGAGAGTATGATTTCTATTTATAGTATTTAACTCGCTTCTCATGACAGATGAA	2278
Q	y	2124	AACAAATATTTTCACATCTCTTTCACAGAGGCTGCTCACTGTCACCAATATCTACAT	2183
D	b	2279	AACAAATATTTTCACATCTCTTTCACAGAGGCTGCTCACTGTCACCAATATCTACAT	2337
Q	y	2184	TGCTGAAAGGCTTTAAATTTCTATGTTCAAGCTTACAGATTTCTGAGGAAATCTA	2243
D	b	2338	TGCTGAAAGGCTTTAAATTTCTATGTTCAAGCTTACAGATTTCTGAGGAAATCTA	2397
Q	y	2244	TATTTTCACTCCCTCAAGACAGTCCATATAAAATTTTCAAGAGCTTGGCTCAATCAAAAT	2403
D	b	2398	TATTTTCACTCCCTCAAGACAGTCCATATAAAATTTTCAAGAGCTTGGCTCAATCAAAAT	2457
Q	y	2304	GATCTCAAGATCAAGATCTTATGATCAATATGCTGAAATCTTGGGCACTTTCTGCAAGTT	23643
D	b	2458	GATCTCAAGATCAAGATCTTATGATCAATATGCTGAAATCTTGGGCACTTTCTGCAAGTT	2517
Q	y	2364	CCAGAAATAAATACATGATGTATGACAGCAAGCTGTGCTTCAAAAGAGCTTTGAAG	24243
D	b	2518	CCAGAAATAAATACATGATGTATGACAGCAAGCTGTGCTTCAAAAGAGCTTTGAAG	2577
Q	y	2424	AAGCAACCTTCTTAAACCACTCAAAAATCTAGCTTTGATATTTCAAGGATTCATCAAGC	24843
D	b	2578	AAGCAACCTTCTTAAACCACTCAAAAATCTAGCTTTGATATTTCAAGGATTCATCAAGC	2647
Q	y	2484	AGATGGAAATTAACATCTCCAGGACAGTCCAAAATTTTACAGAGAACTTGGTCAAAATCAC	25443
D	b	2638	AGATGGAAATTAACATCTCCAGGACAGTCCAAAATTTTACAGAGAACTTGGTCAAAATCAC	2697
Q	y	2544	TTCTTACTCGAATCAATGCTTAAAGTCAAAAATCAATATATGATATATTTCAAAATTA	26043
D	b	2698	TTCTTACTCGAATCAATGCTTAAAGTCAAAAATCAATATATGATATATTTCAAAATTA	2757
Q	y	2604	CCACACAAAATGACATCTTACAGACCTTGGTCCACACTCTGTATACCTTTGATATCTATC	26643
D	b	2758	CCACACAAAATGACATCTTACAGACCTTGGTCCACACTCTGTATACCTTTGATATCTATC	2817

Genome version 5.1.3
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Multiple nucleotide search, using SW model

Run on: January 16, 2003, 15:20:17 : Search time 444 573 Seconds
(without alignments)
17541 794 Million cell updates/sec

Title: US-09-026-459A-40

Perfect score: 4461

Sequence: 1 GGGTCAATGAGGAAAC.....AAATGAGTAATTCATAT 3461

Scoring table:

IDENTITY: NUC

Gapop 10.0 : Gapext 1.0

Search method: 2185249 seps, 1125999159 residues

Total number of hits satisfying chosen parameters: 4 (70478)

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :	N Geneseq	101002:*
1:	US1052/4/quad1a/geneseq/geneseq-emb1/NA1980.DAT:*	
2:	US1052/4/quad1a/geneseq/geneseq-emb1/NA1981.DAT:*	
3:	US1052/4/quad1a/geneseq/geneseq-emb1/NA1982.DAT:*	
4:	US1052/4/quad1a/geneseq/geneseq-emb1/NA1983.DAT:*	
5:	US1052/4/quad1a/geneseq/geneseq-emb1/NA1984.DAT:*	
6:	US1052/4/quad1a/geneseq/geneseq-emb1/NA1985.DAT:*	
7:	US1052/4/quad1a/geneseq/geneseq-emb1/NA1986.DAT:*	
8:	US1052/4/quad1a/geneseq/geneseq-emb1/NA1987.DAT:*	
9:	US1052/4/quad1a/geneseq/geneseq-emb1/NA1988.DAT:*	
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21:	US1052/4/quad1a/geneseq/geneseq-emb1/NA2000.DAT:*	
22:	US1052/4/quad1a/geneseq/geneseq-emb1/NA2001A.DAT:*	
23:	US1052/4/quad1a/geneseq/geneseq-emb1/NA2001B.DAT:*	
24:	US1052/4/quad1a/geneseq/geneseq-emb1/NA2002.DAT:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	Hit ID	Description
1	4461	100.0	4461	19 AAV58447	Modified retinobla
2	4454.8	96.9	4555	19 AAV58440	Modified retinobla
3	4454.8	96.9	4555	19 AAV54990	DNA sequence of th
4	4453.8	96.9	4839	21 AAA29391	Human retinoblasto
5	4453.8	96.9	4839	21 AA288444	Human androgen rec
6	4453.8	96.9	4839	24 AB162873	Breast cancer rela
7	4451.6	96.8	4554	19 AAV58452	Modified retinobla
8	4424.2	96.0	4597	9 AAN81369	Human retinoblasto
9	4424.2	96.0	4597	15 AAQ70546	Human retinoblasto

10	4324.2	96.0	4597	20 AAX04501	Human retinoblasto
11	4322.8	96.0	4740	24 AAN86079	Human retinoblasto
12	4254	94.0	4579	9 AAN81261	Probe for retinobla
13	4247.8	93.8	4455	19 AAV58441	Modified retinobla
14	4228	93.3	4323	19 AAV58446	Modified retinobla
15	4225.4	93.2	4266	19 AAV58434	Modified retinobla
16	4225.4	93.2	4323	19 AAV58443	Modified retinobla
17	4225.4	93.2	4392	19 AAV58442	Modified retinobla
18	4212.4	92.8	4238	15 AAQ72690	Retinoblastoma v4k
19	4212	92.8	4238	15 AAV54991	DNA sequence of th
20	4109	89.8	4347	19 AAV58448	Modified retinobla
21	4107	89.8	4113	19 AAV58445	Modified retinobla
22	2990.4	86.6	4383	19 AAV58451	Modified retinobla
23	2984.4	86.2	4377	19 AAV58450	Modified retinobla
24	2945.2	85.1	5056	10 AAV90489	cDNA of human reti
25	2827.4	81.7	4161	19 AAV58449	Modified retinobla
26	2661.8	76.9	2994	19 AAV4004	Retinoblastoma pro
27	2660.2	76.9	2994	14 AAQ41545	Retinoblastoma gen
28	2650.2	76.9	2594	21 AAQ35287	Wild type human re
29	2658.8	76.8	2995	20 AAX90350	Human p110 RB ret
30	2658.8	76.8	2995	22 AAI25752	Retinoblastoma tum
31	2658.8	76.8	2995	22 AAQ04474	Retinoblastoma tum
32	2658.8	76.8	2995	24 ARL50904	Retinoblastoma tum
33	2658.6	76.8	2994	11 AAQ04713	Cancer suppressing
34	2657.2	76.8	2995	16 AAQ90059	Retinoblastoma tum
35	2655.6	76.7	2995	16 AAQ86498	cDNA encoding a re
36	2652.4	76.6	2995	16 AAQ86498	Human Ret10 cDNA
37	835	24.1	18303	20 AAX04502	Human retinoblasto
38	831.8	24.0	18177	10 AAN90490	DNA of human retin
C 39	220.8	6.4	1698	18 AAI62390	Antisense sequence
C 40	220.8	6.4	1822	18 AAI62397	Effect tandem repe
C 41	220.8	6.4	2631	18 AAI62391	Construct pMK10/AS
C 42	220.8	6.4	4499	18 AAI62393	Construct pMK10/AS
C 43	220.8	6.4	4603	18 AAI62396	Construct pMK10/AS
C 44	218.8	6.3	900	14 AAT01542	Retinoblastoma pro
C 45	218.8	6.3	1697	16 AAT01541	Retinoblastoma pro

ALIGNMENTS

RESULT 1

AAV58447

ID AAV58447 standard; DNA; 4461 bp.

XX AAV58447:

XX Q2-BEC-1998 (first entry)

XX Modified retinoblastoma tumour suppressor gene.

XX Modified retinoblastoma tumour suppressor, K15F protein, cancer therapy;
cellular proliferation inhibitor; ss.

XX Homo sapiens.

XX Key Location/qualifiers

XX CDS 7..2700

XX /*taq- a

XX W09837091.A2.

XX 27-AUG-1998.

XX 19-FEB-1998; 98W0-0S0401.

XX 20-FEB-1997; 97US-0048118.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Benedict WF, Hu S, Xu H, Zhou Y;

DB 478 GAAATCTTAAAGGACATGTCAGATTATATTGACAAAGCCAGCAGT 547
QY 481 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 510
DB 484 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 597
QY 491 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 570
DB 494 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 657
QY 501 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 630
DB 504 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 717
QY 511 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 690
DB 514 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 777
QY 521 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 750
DB 524 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 837
QY 531 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 810
DB 534 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 897
QY 541 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 870
DB 544 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 957
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DB 554 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 1017
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QY 611 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 1290
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DB 624 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 1437
QY 631 TCGATATATACCAAAATACCAATACCAATACCAATACCAATACCAAT 1410
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QY 2551 GTGTTAAATTTAAAGGCTTTTATTTTAAAGGCTTTTATTTTAAAGGCTTT 2610
DB 2638 GTGTTAAATTTAAAGGCTTTTATTTTAAAGGCTTTTATTTTAAAGGCTTT 2697


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CY 2468 TACTCAAGATACAGAACTCTAGTATCAATTTGGTCAATCAATGGGACATCTGAGAAAGTT 2447
DB 2468 GACTCCAGATCAGAAATCTTATATATATATATATATATATATATATATATATATATATAT 2517
CY 2468 GTAGAAATATAATATATATATATATATATATATATATATATATATATATATATATATAT 2507
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DB 2468 AAGCAATATATATATATATATATATATATATATATATATATATATATATATATATAT 2637
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DB 2468 AAGCAATATATATATATATATATATATATATATATATATATATATATATATATATAT 2877
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RESULT 13
AAV58441
ID AAV58441 standard; DNA; 3455 BP.
XX
XX AAV58441;
XX
XX 02-DIC-1998 (first entry)
XX
XX Modified retinoblastoma tumour suppressor gene.
XX
XX Modified retinoblastoma tumour suppressor, RBP protein; cancer therapy;
XX cellular proliferation inhibitor; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 7..2694
XX /tag= a
XX
XX W09837091-A2.
XX
XX 27-AUG-1998.
XX
XX 19-FEB-1998; 98W0-US03041.
XX
XX 20-FEB-1997; 970S-0038118.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Benedict WF, Hu S, Xu H, Zhou Y;
XX
XX WPI: 1998-480788/41.
XX P-PSDB: AAW69365.
XX
XX Retinoblastoma suppressor protein with N-terminal modification -
XX inhibiting cellular proliferation, particularly cancer
XX
XX Claim 22; Page 142 147, 249pp; English.
XX
XX This sequence encodes a modified retinoblastoma tumour suppressor
XX protein (RBP) of the invention. The proteins can be used for inhibiting
XX cellular proliferation, when coadministered with a p53 protein. The RBP
XX can be used for treating diseases characterised by abnormal cellular
XX proliferation, particularly cancers. The RBP has a broader spectrum of
XX activity than wild type RBP.
XX
XX Sequence 3455 BP; 1153 A; 631 C; 627 G; 1044 I; 0 other;

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Query Match 93.8%; Score 3247.8; DB 19; Length 3455;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 3352; Conservative 0; Mismatches 2; Indels 93; Gaps 1;
CY 108 GAGGACATAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 167
DB 108 GAGGACATAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 167
CY 168 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 68
DB 168 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 68
CY 168 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 227
DB 168 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 227
CY 168 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 128
DB 168 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 128
CY 228 TTGGTTG----- 244
DB 228 TTGGTTG----- 244
CY 129 TTGGTTGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 188
DB 129 TTGGTTGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 188
CY 235 -----GTCGACCTAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 254
DB 235 -----GTCGACCTAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 254
CY 189 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 248
DB 189 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 248
CY 255 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 314
DB 255 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 314
CY 249 GTTCACATTTTACTGAGCTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 408
DB 249 GTTCACATTTTACTGAGCTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 408

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14 2420 AAAGAGAAACCCGACAAAACGCGCCGACGATGCTCCAAATGCAATTCATTCAGCTG 2979
15 3175 GGCATTCACGAAATATCTGAACTCTGCGAAMATGGATATATTAGAAATTAGAA 3234
16 2980 GCGAATGACGAAATATCTGAACTCTGCGAAMATGGATATATTAGAAATTAGAA 3039
17 3235 AAAAAATACGAAATATGACATATAGATTTATTTACTATGCGAAATGATATACGCTG 3294
18 3040 AAAAAATATATTTTACATATAGATTTATTTACTATGCGAAATGATATACGCTG 3099
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20 3159 GCTTGTTTTATAAAAATTTGCTTTTAAATTAATAAAGCTGGAAGCAAGATATAACCA 3159
21 3455 TGATATATATATATATATGAAATGATTTGATATCTGCAATGTAAAGAACTTACTGAT 3414
22 3160 TGATATATATATATATGAAATGATTTGATATCTGCAATGTAAAGAACTTACTGAT 3219
23 3455 TATTTGCGATGCAACTTATGTTTTAAATGAGGATATATGATAGT 3461
24 3423 TATTTGCGATGCAACTTATGTTTTAAATGAGGATATATGATAGT 3266
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Search completed: January 16, 2003, 23:28:23
Job time: 184.57s

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

LE $\frac{d}{dt} \log \left(\frac{\|x\|}{\|y\|} \right) = -\frac{1}{2} \frac{\langle x, y \rangle}{\|x\|^2 \|y\|^2}$

XX W0847091.A2.
 XX 27-AUG-1998.
 XX 19 FEB-1998; 98W0-US03041.
 XX 20 FEB-1997; 97US-0038118.
 XX (HAYO) HAYLOR COLLEGE MEDICINE.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Benedict WF, Hu S, Xu H, Zhou Y;
 XX W011998.486788/41.
 XX P-DSDB; AAW69471.
 XX
 XX Retinoblastoma suppressor protein with N-terminal modification -
 XX inhibiting cellular proliferation, particularly cancer
 XX
 XX Cn3im 22; Page 188 192; 249pp; English.
 XX this sequence encodes a modified retinoblastoma tumor suppressor
 XX protein (R1SP) of the invention. The proteins can be used for inhibiting
 XX cellular proliferation, when administered with a p53 protein. The p53ps
 XX can be used for treating diseases characterized by abnormal cellular
 XX proliferation, particularly cancers. The R1SPs have a broader spectrum of
 XX activity than wild type R1SPs.
 XX
 XX Sequence 4461 BP; 1141 A; 675 C; 627 G; 1018 T; 0 other;
 XX
 XX Alignment Scores:
 XX Fred. No.: 0 Length: 3461
 XX Score: 4631.00 Matches: 897
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX ID: 19 Gaps: 0
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 XX us-09-026-459a-41 (1-897) x AAW58447 (1-3461)
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 XX 7 ALISVSGVAAANVCGCTGCAAAAANVGGVAGVAGVAGVAGVAGVAGVAGVAGV 66
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 XX 21 ProAlaProProProProProProProGluGluAspProGluGluAspSerGlyProGlu 40
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 XX 47 GGGGAG 126
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 XX 41 AspLeuProLeuValAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
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 XX 127 GAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 186
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 XX 41 CysGlnLysLeuLysIleProAspHisValArgGluArgAlaTrpLeuValAspLeu 80
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 XX 187 TGTCAAGAAATTAACATACATACATACATACATACATACATACATACATACAT 246
 XX
 XX 81 GluMetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhe 100
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 XX 247 GAGATGTGGTCACTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 306
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 XX 141 PheAlaLeuLeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLeu 120
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 QY 291 ProMetLeuLeuLysCysLeuLeuLeuLysTrpAlaValIleGlnCysGlnLysPheArg 420
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 QY 607 CCAATGTTGCTCAAGCAATCAATAAAAGTGGTGGTGGTGGTGGTGGTGGTGGT 466
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QY 400 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly 509
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 D 1999 GTTCAATGATCACTTGAATCTGCTGCTTGAATCTGCTGCTTGAATCTGCTGCTTGAAT 2058
 QY 690 ProLeuLysSerThrSerLeuSerLeuPheTyrLysValTyrArgLeuAlaTyrLeu 629
 D 2059 AATGCAATGATCACTTGAATCTGCTGCTTGAATCTGCTGCTTGAATCTGCTGCTTGAAT 2118
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 QY 690 PheLysIleLeuValThrAlaTyrLysAspLeuProHisAlaValGlnGlnThrPheLys 709
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 D 2599 GTTCAATGATCACTTGAATCTGCTGCTTGAATCTGCTGCTTGAATCTGCTGCTTGAAT 2658
 QY 810 ThrSerGlnLysPheGlnLysThrAsnGlnMetValCysAspSerAspArgValLysLys 829
 D 2659 GTTCAATGATCACTTGAATCTGCTGCTTGAATCTGCTGCTTGAATCTGCTGCTTGAAT 2718
 QY 830 ArgSerAlaLeuLysSerAspProProLysProLeuLysLysLysLysLysLysLys 849
 D 2719 GTTCAATGATCACTTGAATCTGCTGCTTGAATCTGCTGCTTGAATCTGCTGCTTGAAT 2778

QY 850 GlySerAspGluAlaAspCysLysSerLysHisLeuProSerLeuSerLysPheGlnGlnLys 869
 D 2779 GTTCAATGATCACTTGAATCTGCTGCTTGAATCTGCTGCTTGAATCTGCTGCTTGAAT 2838
 QY 870 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 889
 D 2839 GTTCAATGATCACTTGAATCTGCTGCTTGAATCTGCTGCTTGAATCTGCTGCTTGAAT 2898
 QY 890 AspThrSerAsnLysGluGluLys 897
 D 2899 GTTCAATGATCACTTGAATCTGCTGCTTGAATCTGCTGCTTGAATCTGCTGCTTGAAT 2922
 RESULT 6
 ID AAH25755 standard; DNA; 2995 BP.
 XX AAH25755:
 XX 14-AUG-2001 (first entry)
 XX Retinoblastoma tumour suppressor gene.
 XX Retinoblastoma: tumour suppressor protein; P53; cancer;
 XX adenoviral vector; gene therapy; thymidine kinase; ds.
 XX Unidentified.
 XX US-09-026-459a-41.
 XX 05-JUN-2001.
 XX 24-NOV-1999; 99US-0449113.
 XX 25-OCT-1994; 94US-0328673.
 XX 25-OCT-1994; 94US-0142669.
 XX 19-MAY-1994; 94US-0246006.
 XX (GREGG) GREGORY R J.
 XX (WILLI) WILLS K N.
 XX (MANE/) MANEVAL D C.
 XX Gregory RJ, Wills KN, Maneval DC;
 XX WP: 2001-49/239/42.
 XX P-PSDB: AAB98945.
 XX Recombinant adenovirus expression vector comprising a partial or total
 XX deletion of a protein IX DNA and a gene encoding a foreign protein e.g.
 XX suicide protein, useful for inhibiting or reducing the proliferation of
 XX a tumour e.g. brain tumour -
 XX Disclosure: Fig 3; 39pp; English.
 XX The present invention describes an adenoviral expression vector
 XX comprising a deletion in the protein IX gene and a gene encoding a
 XX foreign protein. This vector can be used in gene therapy, particularly to
 XX introduce tumour suppressor genes into tumorous cells. Genes which may
 XX be used include p53, thymidine kinase and retinoblastoma tumour
 XX suppressor gene (Rb). The present sequence is the retinoblastoma tumour
 XX suppressor gene.
 XX Sequence 2995 bp; 975 A; 614 C; 594 G; 809 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 2995
 Score: 4605.50 Matches: 897
 Percent Similarity: 96.56% Conservative: 0
 Best Local Similarity: 96.66% Mismatches: 0
 Query Match: 99.45% Indels: 31
 DB: 22 Gaps: 1
 US-09-026-459a-41 (1-897) x AAH25755 (1-2995)

27 440 SerThrSerThrAsnLeuAspSerGlyThrAspLeuSerPheProThrPheLeuAsnVal 489
 14 1507 AATAATATCTCAAAATCTGATGCTGAGAACATTTGGCTTTCGATGATGATTTGTAATGTG 1566
 27 490 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGlnSerPheIleLysAlaGlnGly 509
 14 1567 GTTAAATTTAAAGGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1626
 27 510 AsnLeuThrArgGlnMetIleLysHisLeuGlnArgGlySerGlnHisLeuMetGlnSer 529
 14 1627 AATTTCAAG 1686
 27 540 LeuAlaIlePheLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 549
 14 1687 CTGCAAG 1746
 27 560 GlyProThrAspHisLeuGlnSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 569
 14 1747 GATCAAG 1806
 27 570 ThrAlaAlaAspMetIleLeuSerProValArgSerProLysLysLysGlySerThrThr 589
 14 1807 ATTCAG 1866
 27 590 ArgValAsnSerThrAlaAsnAlaGlnThrGlnAlaThrSerAlaPheGlnThrGlnLys 609
 14 1867 GATCAAG 1926
 27 610 ProLeuLysSerThrSerLeuSerProPheTyrLysValIleLeuAlaTyrLeu 629
 14 1927 GATCAAG 1986
 27 640 ArgLeuAsnThrLeuGlySerArgLeuLeuSerGlnHisProGlnLeuGlnHisIleIle 649
 14 1987 GATCAAG 2046
 27 650 TrpThrLeuPheGlnHisThrLeuGlnAsnGlnIleTyrGlnLeuMetArgAspArgHisLeu 669
 14 2047 TCAAG 2106
 27 670 AspIleIleMetCysSerMetTyrGlyIleLysLysValLysAsnIleAspLeuLys 689
 14 2107 GATCAAG 2166
 27 690 PheLysIleIleValThrAlaIleLysAspLeuProHisAlaValGlnGlnThrPheLys 709
 14 2167 TTTCAAG 2226
 27 710 ArgValIleIleLysGlnGlnIleTyrAspSerIleIleValPheTyrAsnSerValPhe 729
 14 2227 GATCAAG 2286
 27 740 MetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProThrLeuSer 749
 14 2287 ATTCAG 2346
 27 750 ProIleProIleProArgSerProTyrLysPheProSerProLeuArgIlePro 769
 14 2347 TTTCAAG 2406
 27 770 GlyLysAsnIleIleSerProLeuLysSerProTyrLysIleSerGlnGlyLeuPro 789
 14 2407 GATCAAG 2466
 27 790 ThrProThrLysMetThrProArgSerArgIleLeuValSerThrGlyLysPheGly 809
 14 2467 ATTCAG 2526
 27 810 ThrSerGlnLysPheGlnGlnIleAsnGlnMetValLysAsnSerAspArgValIleLys 829
 14 2527 ATTCAG 2586
 27 830 ArgSerAlaGlnLysSerAsnProThrLysProLeuLysLeuArgPheAspIleGln 849

DB 2587 ACAAGTCTGAAGGAAGCAAGCCCTCCCTAAACACACGAAAAACCTACGCTTTCATATGAA 2646
 QY 850 GlySerAspGlnAlaAspGlySerLysHisLeuProGlyGlySerLysPheGlnGlnLys 869
 DB 2647 GCATTCATCAGCAAGGACAGATGGAAGTAACATATCCATGACAGAGTCCAAATTTTCAGTCAAAA 2706
 QY 870 LeuAlaGlnMetThrSerThrArgMetGlnLysGlnLysMetAspAspSerMet 889
 DB 2767 CTGGGTAAAAATGCTTCTACTGAAATGAAATGTAATGTAATGTAATGTAATGTAATGTAATG 2766
 QY 890 AspThrSerAsnLysGlnGlnLys 897
 DB 2767 CATACCTCAACCAAGCAAGACAGAAA 2790
 RESULT 10
 ID AAV54990 standard; DNA: 3555 BP.
 XX AAV54990;
 DT 26-NOV-1998 (first entry)
 XX DNA sequence of the specification.
 XX Minimal promoter; tetracycline responsive expression vector; PREV;
 KW transcriptional transactivation domain; TTD;
 KW tetracycline repressor protein; TRP; tetracycline operator;
 KW production, stable cell line; protein production;
 KW tumour suppressor protein; treatment; cancer; SS.
 XX Unidentified.
 XX Key Location/Qualifiers
 FT CDS 7..2793
 FT /*tag- a
 XX WO9837185-A2.
 PD 27-AUG-1998.
 PF 19-FEB-1998; 98WO-US03092.
 PR 20-FEB-1997; 97US-0038755.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PI Hu S, Logothetis CJ, Xu H, Zhou Y;
 DR WPI: 1998-480796/41.
 DR P-PSDB: AAW71354.
 XX New tetracycline responsive expression vectors used for the
 PT tightly controlled expression of genes, such as tumour suppressor
 PI genes for treating cancers
 XX Disclosure: Pages 145-159; 190pp; English.
 CC The present sequence appears in the specification, which describes a
 CC tetracycline responsive expression vector (PREV), which contains a
 CC sequence encoding a fusion protein comprising a transcriptional
 CC transactivation domain (TTP) operatively attached to a tetracycline
 CC repressor protein (TRP). The first sequence operatively positioned
 CC downstream of a promoter. The vector also contains a cloning site
 CC operatively positioned downstream of a basal promoter comprising a
 CC tetracycline operator. The PREVs can be used to produce stable cell
 CC lines in which gene expression is tightly regulated by tetracycline.
 CC They can be used for the production of proteins such as tumour
 CC suppressor proteins which can be used for treating diseases characterised
 CC by abnormal cellular proliferation, particularly cancers.
 XX Sequence 3555 BP; 1171 A; 684 C; 654 G; 1047 T; 0 other;

[illegible]

QY	B10	ThrsrGlnLysPheClnLysIleAsnGlnMetValLeuSAsnSerASPATgAlloLys	829
D6	2659	ACTTCTGAAGATCCAGAAAATAAATAGATGGTAGTGTAACAGAGACCCTGTGTGTCAA	2718
QY	830	AATSerAlaCLeuGlySerAsnProLeuPisProLeuLysLysLeuAlaGluAspLeuGlu	849
D6	2719	AGAAGTCTCAAGGAGCACCCCTCTAAACCATCGAAAAACTACGCCTTCGATTACAA	2778
QY	850	GlySerAspGluAlaAspGlySerLysHisLeuPheGlyGluSerLysPheGlyGluLeuS	869
D6	2779	CGATCAGATCAACGACAGATCGAACTAAACAATCTCCACAGAGACATCCAAAATCACGACAGAA	2848
QY	870	IcuAlaGluMetThrSorlthrArgThrArgMetGlnLysClnLysMetAspSerMet	894
D6	2839	CTGGACGAAATGATTTTATTCTGAACATCAATGCAAAATGCAAAATGAAATGATAGCATG	2898
QY	890	AspThrSerAsnLysGluGluLys	897
D6	2899	CATACCTCAACCAACGACAGAGAAA	2922
RESULT 15			
AAQ04713			
ID	AAQ04713 standard; cDNA; 2994 bp.		
AC	XX	AAQ04713;	
DT	XX	11-OCT-1990 (first entry)	
DE	XX	Cancer suppressing gene (CSG).	
KW	XX	Cancer; cancer suppressing gene; CSG; 13q14; retinoblastoma;	
KW	XX	RB; ds.	
GS	XX	Homo sapiens.	
FH	XX	key location/qualifiers	
FT	XX	139..2922	
FT	XX	/tag= a	
XX	XX	W09005180-A.	
XX	XX	17-MAY-1990.	
XX	XX	60-EVT-1989; H460-0004808.	
XX	XX	41-EVT-1988; HRTS-0255x29.	
PA	XX	(RECC) UNIV OF CALIFORNIA.	
PI	XX	Lee WH, Huang HJS;	
CE	XX	WHJ: 1990-178x22/23.	
DR	XX	p-PSDB; AAR05305.	
PT	XX	Controlling cancer -	
PT	XX	by replacing ineffective cancer suppressing gene with cloned,	
PT	XX	active gene.	
PS	XX	Claim 35; Page 86; 105pp; English.	
XX	XX	Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.	
CC	XX	By installing a working CSG, safe and specific treatment and	
CC	XX	prophylaxis can be given to cancer patients.	
XX	XX	Sequence 2994 bp; 974 A; 618 C; 593 G; 809 T; 0 other;	
Alignment Scores:			
Pred. No.:	0	Length:	2994
Score:	4596.50	Matches:	896
Percent Similarity:	97.6%	Conservative:	0
Best Local Similarity:	96.55%	Mismatches:	1
Query Match:	99.26%	Indels:	31

[illegible]

	Db	1159	AAACCTCTTCAGACTGATCTCATAGACAGTTTGGAAA'ACACAGAACAA'CA'AAAAAAGC	1218
QY	330	AsnLeuAspGluGlnValAsnValIleProPheHisThrProValArgThrValMetAsn		449
Db	1219	AACCTTTGATCAAGACGGTGGAAGAATCTGTCCA'ACA'TCCAGTAGACACTCTATCAA'	1278	
QY	350	ThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 69		
Db	1279	ACTATGCCAA'CAATTAATGATGATTATAATTC'ACG'AATGTGATCAAC'CTTCAAAATCTG	1348	
QY	370	IleSerTyrPheAsnAsnCysThrValAsnProTyrYSGLuSetIleLeuLysArgValLys	389	
Db	1339	ATTTCCTATTTTAACCACTGCACAGTGAATCT'AAAAAGAAACATACT'GAAACAGACTGAAT	1498	
QY	390	AspIleGlyTyrIlePheLysGlnLysPheAlaLysAlaValGlyGlnGlycysValGln	409	
Db	1399	GATATAGGATACATCTTTAAACAGAGAACTUGCT'AAAGCTGGCGCA'ADGGTGGTCCAA	1458	
QY	410	IleGlySerGlnArgTyrIleLysGlnGlyValAlaValcysTyrTyrArgValMetCysSerMet	429	
Db	1459	ATTGGATACACGGGATACAAATTTGAGATTCCTGTATATAC'GAGTAGTAATPGAAATCATG	1518	
QY	430	LeuLysSerGlnGluGluArgLeuSerIleGlnAsnProSerLysLeuLeuAsnAspAsn	449	
Db	1519	CCTTAAATCACAGAACAAACGATATCCATCT'AAAAATTAAG'AAACCTTCACATCA'AA'	1578	
QY	450	IlePheHisMetSerLeuLeuAlacysAlaLeuGluValValMetAlaThrTyrSerArg	469	
Db	1579	ATTCTTCATATGTCCTTTATGGCGTGCGCTCTGGAGTGGTAAGCG'ACAAATATAGAGA	1638	
QY	470	SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnVal	489	
Db	1639	AGTACATCTAGAACTTGATCTGACACACAAATTGTCTTCCATCGATTTCAATCTG	1698	
QY	490	LeuAsnLeuLysAlaPheAspPheTyrLysValIleGlnSerPheIleLysAlaGlnGly 509		
Db	1699	CCTTAATTTAAAGCCCTTGATTTTTACAAGAGCATCGAAAGTTTAT'CAAAAG'CAAAAG'	1758	
QY	510	AsnLeuThrArgGlnMetIleLysHisLeuGluArgCysGlnHisArgIleMetGlnSer	529	
Db	1759	AACHCACAGACAAAAGAAACAACTTACAACTAGTGGACATCGAAATCAAGAAATCT	1818	
QY	530	LeuAlaTripleSerAspSerProLeuPheAspPheIleLysGlnSerLysAspArgGln 549		
Db	1819	CTTGATGGCTCTCAGATTCAGCTTATTATGATCTTATTAAACAAT'AAAGAACTCAAA	1878	
QY	550	GlyProThrAspHisLeuGlnSerAlaLysProLeuAsnLeuProLeuGlnAsnHis 569		
Db	1879	GGACCACATCATCACCCTGCAATCTGCTGTGCTCTTAATCTCTCTCTCAAAATAC'	1938	
QY	570	ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysSerThrThr 589		
Db	1939	ACTCCAGCCATATGATATCTTCTCTGCTAACATCTCC'AAAAACAAAAAAGTTCAATACG	1998	
QY	590	ArgValAsnSerThrAlaAsnAlaGlnIleArgGlnAlaIleSerAlaPheGlnIleGlnLys 609		
Db	1999	CGTGTAATTTCTACTG'AAATGCAAGAGCA'AAAGCAACCTTAGGCTTC'CAACATCAAAAG	2058	
QY	610	ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrAlaLeuAlaTyrLeu	629	
Db	2059	CCATTCAAAICTACCTCTCTTCACCTGTTTATAAAAAAGAGTATCGGTAAGCT'ATCTC	2118	
QY	630	ArgLeuAsnThrLeuCysGlnArgLeuLeuSerGlnHisProGlnLeuGlnHisIleIle 649		
Db	2119	CGGCTAAATACACTTGTGAAGCGGCTCTGCTGAGCACTCAAGATACAA'ATATATAC	2178	
QY	650	TrpIleLeuPheGlnHisThrLeuGlnAsnGlnTyrGlnLeuMetArgAspArgHisLeu	669	
Db	2179	TGACACCTTTTCAAGCA'ATGCTGCAAGAAATAGCATGAAATATAGAGA'ATAGCTATTTG	2238	
QY	670	AspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspGlnLys	689	

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ORF nucleic nucleic search using sw model

Run on: January 16, 2003, 15:20:17 : Search time 429.93 Seconds
(without alignments)
17541.794 Million cell updates/sec

Title: US 09 026 459A 42

Product score: 447

Sequence: 1 GGGGTATGCGGCAAAAC.....AATGAGATATTGATAGT 4347

Seed tag table: IDENTITY.ND

Gapop 10.0 : Gapext 1.0

Searched: 2185249 seqs 1125690159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 9%

Maximum Match 100%

Listed first 45 summaries

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24:	3	SIUS22/ncubata/geneseq/geneseq-emb1/NA2002.DAT*	

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	4447	100.0	4347	19	AAV58448 Modified retinoblastoma
2	4126.8	93.4	4554	19	AAV58452 Modified retinoblastoma
3	4126.8	93.4	4555	19	AAV58440 Modified retinoblastoma
4	4126.8	93.4	4555	19	AAV54990 DNA sequence of th
5	4125.8	93.4	4839	21	AAA25991 Human retinoblasto
6	4125.8	93.4	4839	21	AAZ88444 Human androgen rec
7	4125.8	93.4	4839	24	ARL62873 Breast cancer rela
8	4114.6	93.1	4740	24	ARK66079 Human retinoblasto
9	4111	92.9	4377	19	AAV58450 Modified retinoblasto

10	4109	92.9	3461	19	AAV58447 Modified retinoblasto
11	4096.2	92.5	4597	15	AAV70536 Human retinoblasto
12	4096.2	92.5	4597	20	AAV04501 Human retinoblasto
13	4094.6	92.5	4597	9	AAH1369 Human retinoblasto
14	4066.2	91.6	3323	19	AAV58446 Modified retinoblasto
15	4042.4	90.6	4579	9	AAH1261 Probe for retinoblasto
16	4019.8	90.2	3455	19	AAV58441 Modified retinoblasto
17	4006	89.8	3114	19	AAV58445 Modified retinoblasto
18	4006	89.8	3218	19	AAV54991 DNA sequence of th
19	4006	89.8	3266	19	AAV58444 Modified retinoblasto
20	4006	89.8	3323	19	AAV58443 Modified retinoblasto
21	4006	89.8	3392	19	AAV58442 Modified retinoblasto
22	2993.4	89.4	3234	15	AAV70536 Human retinoblasto
23	2965	88.6	3161	19	AAV58449 Modified retinoblasto
24	2946.6	88.0	5056	10	AAV58449 Modified retinoblasto
25	2911.4	87.0	3383	19	AAV58451 Modified retinoblasto
26	2433.8	72.7	2994	19	AAV40004 Retinoblastoma pro
27	2432.2	72.7	2994	14	AAV41545 Retinoblastoma pro
28	2432.2	72.7	2994	21	AAV40004 Retinoblastoma pro
29	2430.8	72.6	2995	20	AAV50350 Wild type human re
30	2430.8	72.6	2995	22	AAH25755 Human p110 RB reti
31	2430.8	72.6	2995	22	AAH25755 Retinoblastoma tum
32	2430.8	72.6	2995	23	AAH25755 Retinoblastoma tum
33	2430.6	72.6	2994	11	AAV04713 Retinoblastoma tum
34	2429.2	72.6	2995	16	AAV50359 Cancer suppressio
35	2427.6	72.5	2995	20	AAV50359 Retinoblastoma tum
36	2424.4	72.4	2995	16	AAV50359 cDNA encoding a re
37	835	24.9	18303	20	AAV04502 Human retinoblasto
38	831.8	24.9	18177	10	AAV04502 DNA of human reti
39	220.8	6.6	1698	18	AAV62396 Adipocyte sequence
40	220.8	6.6	1802	18	AAV62396 Direct tandem repe
41	220.8	6.6	2834	18	AAV62396 cDNA of PKC17AS
42	220.8	6.6	3493	18	AAV62396 cDNA of PKC17AS
43	220.8	6.6	4031	18	AAV62396 cDNA of PKC17AS
44	218.8	6.5	909	16	AAV01542 Retinoblastoma pro
45	218.8	6.5	1697	18	AAV01542 Retinoblastoma pro

ALIGNMENTS

RESULT 1

AAV58448

ID AAV58448 standard; DNA; 4347 bp.

AC AAV58448;

XX 02-DEC-1998 (first entry)

XX Modified retinoblastoma tumour suppressor gene.

XX Modified retinoblastoma tumour suppressor gene.

XX Cellular proliferation inhibitor; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 7..2586

XX FT /*tag- a

XX W09837091-A2.

XX 27-AUG-1998.

XX 19-FEB-1998; 98W0-US03041.

XX 20-FEB-1997; 97US-0048118.

XX (HAYU) HAYUOK COLLEGE MEDICINE.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Benedict WF, Hu S, Xu H, Zhou Y;

XX


```

DB 2041 AATCTGACAGGCTTTTTCATCAACACAGCTGCAGAAATGAGTAAGAAATCATCAGACAGAG 2100
      |||
QY 1894 CATTGTGACCAAAATATGATGTTGCTGATGATGCTATGCTCAAGATGAGAAATATATAGAC 1953
      |||
DB 2100 CATTGTGACCAAAATATGATGTTGCTGATGATGCTCAAGATGAGAAATATATAGAG 2160
      |||
QY 1954 GTTAAATTCAAAATTCATGATGATGCTGATGCTCAAGATGAGAAATATATAGAG 2013
      |||
DB 2161 GTTAAATTCAAAATTCATGATGATGCTGATGCTCAAGATGAGAAATATATAGAG 2220
      |||
QY 2014 TTTAAATTCAAAATTCATGATGATGCTGATGCTCAAGATGAGAAATATATAGAG 2073
      |||
DB 2221 TTTAAATTCAAAATTCATGATGATGCTGATGCTCAAGATGAGAAATATATAGAG 2280
      |||
QY 2074 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2133
      |||
DB 2281 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2340
      |||
QY 2134 TTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2193
      |||
DB 2341 TTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2400
      |||
QY 2194 ATCTGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2253
      |||
DB 2401 ATCTGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2460
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QY 2254 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2313
      |||
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      |||
QY 2314 TTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2373
      |||
DB 2521 TTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2580
      |||
QY 2374 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2433
      |||
DB 2581 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2640
      |||
QY 2434 ATTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2493
      |||
DB 2641 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2700
      |||
QY 2494 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2553
      |||
DB 2701 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2760
      |||
QY 2554 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2613
      |||
DB 2761 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2820
      |||
QY 2614 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2673
      |||
DB 2821 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2880
      |||
QY 2674 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2733
      |||
DB 2881 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2940
      |||
QY 2734 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2793
      |||
DB 2941 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3000
      |||
QY 2794 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2853
      |||
DB 3001 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3060
      |||
QY 2854 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2913
      |||
DB 3061 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3120
      |||
QY 2914 GTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 2973
      |||

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DB 3121 CTTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3180
      |||
QY 2974 TAAATTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3033
      |||
DB 3181 TAAATTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3240
      |||
QY 3034 ATCTGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3093
      |||
DB 3241 ATCTGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3300
      |||
QY 3094 AAAATTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3153
      |||
DB 3301 AAAATTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3360
      |||
QY 3154 TTAATTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3213
      |||
DB 3361 TTAATTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3420
      |||
QY 3214 AAAATTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3273
      |||
DB 3421 AAAATTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3480
      |||
QY 3274 CCTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3333
      |||
DB 3481 CCTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3540
      |||
QY 3334 GCTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3393
      |||
DB 3541 GCTTCATGACAGACAGTCAAAATTAATATTTTTCAGTATGCTTCCCAACAGGCTGCTAGG 3600
      |||

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RESULT 4

AAV54990

ID AAV54990 standard; DNA: 4555 BP.

XX AAV54990;

XX 26-NOV-1998 (first entry)

XX DNA sequence of the specification.

XX Minimal promoter; tetracycline responsive expression vector; IRV;

XX Transcriptional repressor protein; TRP;

XX Tetracycline repressor protein; TRP; tetracycline operator;

XX Production; stable cell line; protein production;

XX Tumour suppressor protein; treatment; cancer; ss.

XX Unidentified.

XX Key location/qualifiers

XX CDS 7..2793

XX /*laq= a

XX W09847185-A2.

XX 27-AUG-1998.

XX 19-FEB-1998; 98W0-050492.

XX 20-FEB-1997; 97US-0048755.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Hu S, Logothetis CJ, Xu H, Zhou Y;

XX WPI; 1998-480796/41.

XX P-PSDR; AAW71354.

XX New tetracycline responsive expression vectors - used for the
 XX tightly controlled expression of genes, such as tumour suppressor
 XX genes for treating cancers

PS Disclosure; Pages 145-150; 190pp; English.

DB 478 GAAATTTTACGAAATTTGAAAGGACATGAGAACTTAAATATATGACATCAAGCAGCAGT 537
QY ATCTAGTAATTAATTTGGATTGCTGTAAAGATTTTCTTGATCATCATTTTAA 396
DB 479 GCAATATATCAATGAAATTAATATGATGCTGCTAAAGATTTTCTTGATCATCATTTTAA 597
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 456
DB 480 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 657
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 516
DB 481 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 717
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 576
DB 482 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 777
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 636
DB 483 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 837
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 696
DB 484 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 897
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 756
DB 485 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 957
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 816
DB 486 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1017
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 876
DB 487 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1077
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 936
DB 488 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1137
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 996
DB 489 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1197
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1056
DB 490 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1257
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1116
DB 491 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1317
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1176
DB 492 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1377
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1236
DB 493 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1437
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1296
DB 494 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1497
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1356
DB 495 TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1557
QY TAAATTAAGAGGAGAGATTAATTAAGAGGAGATGCTGCTGATTTTCTTGATTTTAA 1416

DB 1558 GTGCTTAATTTTAAAGGCTTTTGTGATTTTAAAGAGATGATCAAGAGCTTTTAA 1617
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1476
DB 1559 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1677
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1536
DB 1560 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1737
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1596
DB 1561 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1797
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1656
DB 1562 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1857
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1716
DB 1563 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1917
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1776
DB 1564 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1977
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1836
DB 1565 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2037
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1896
DB 1566 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2097
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 1956
DB 1567 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2157
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2016
DB 1568 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2217
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2076
DB 1569 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2277
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2136
DB 1570 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2337
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2196
DB 1571 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2397
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2256
DB 1572 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2457
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2316
DB 1573 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2517
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2376
DB 1574 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2577
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2436
DB 1575 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2637
QY GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2496
DB 1576 GGAAGTTGATCAAGAGAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAA 2697

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2497 AAAATGGAGAAATGACCTTCTACTGACACAGCAATGCAAAAGCAGAAAATGAATGATAGC 2556
2498 AAACAGGCAAAAGACCTTCTACTGACACAGCAATGCAAAAGCAGAAAATGAATGATAGC 2557
2499 ATGATAGCTAAATGAAGCAAGCAATGAAGCAAGCAATGAAGCAAGCAATGAAGCAAGCA 2616
2500 ATGATAGCTAAATGAAGCAAGCAATGAAGCAAGCAATGAAGCAAGCAATGAAGCAAGCA 2617
2501 CACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2676
2502 CACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2677
2503 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2746
2504 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2747
2505 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2937
2506 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2938
2507 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2996
2508 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2997
2509 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2856
2510 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2857
2511 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3057
2512 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3058
2513 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3117
2514 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3118
2515 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2976
2516 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3177
2517 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3036
2518 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3237
2519 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3238
2520 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3096
2521 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3207
2522 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3156
2523 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3357
2524 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3216
2525 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3417
2526 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3276
2527 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3477
2528 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3336
2529 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3537
2530 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3347
2531 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3548
2532 IGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

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XX OS Homo sapiens.
XX Key: location/Qualifiers
XX CDS 337..2787
XX FT /*tag= a
XX PN EP259031-A.
XX RD 09-MAR-1988.
XX XX 11-AUG-1987; WHP-007095.
XX XX 11-AUG-1986; BUDS-0895163.
XX (MASS-) MASSACHUSETTS EYE.
XX (WHIT-) WHITEHEAD INST BIOMED RES.
XX Dryja TP, Friend S;
XX WPI; 1988-065827/10.
XX P-PSDB; AAP82112.
XX Diagnosis of retinoblastoma - using genetic material corresp. to a normal
XX human retinoblastoma gene or a unique sub-region
XX Disclosure; ; p; English.
XX This gene encodes a protein, the absence of which is associated with a
XX retinoblastoma. It is used to produce an antibody to the protein, contacting
XX this with the tumour sample and detecting immune complexes as indication
XX of the presence in the tumour sample of the protein. Whole sequence or
XX a unique sub-region can be used. The method identifies patients lacking
XX the defective retinoblastoma (Rb) allele and thus are not at risk of
XX developing the disease.
XX Sequence 4597 BP; 1489 A; 899 C; 615 G; 1454 T; 0 other;

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Query Match 92.5%; Score 3094.6; DB 9; Length 4597;
Best Local Similarity 94.0%; Pct. Id. 0;
Matches 3337; Conservative 0; Mismatches 4; Indels 210; Gaps 3;
QY 4 GTATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63
DB 1 GTATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 64 GTATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 123
DB 61 GTATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 118
QY 124 GATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
DB 119 GATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 177
QY 184 TTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
DB 178 TTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 237
QY 244 AAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
DB 238 AAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
QY 304 GGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 341
DB 298 GGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
QY 342 ----- 341
DB 358 CTACAGAAAACATACAGAAAATCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
QY 342 ----- 341
DB 418 ACCATATATATATATATATATATATATATATATATATATATATATATATATATATAT 477

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RUSHT 13
AARH 13
XX AARH 13; standard; DNA; 4597 BP.
XX AARH 13;
XX 22 Oct 1990 (first entry)
XX Human retinoblastoma gene.
XX Retinoblastoma; neoplasm, osteosarcoma, ss.

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QY 342 341
DB 476 GAAATGTTGCAAAAGGACATGTGAAATTATATATTGAAAGGACAGCACT 537
QY 342 AATACATCAAAATAATCTGCAATGCGATGAAAGGATGCAATCAATTTTAA 396
DB 346 GAGATATATATGAAATAATGCGATGCGGATGAAAGGATGCGATGCAATTTTAA 597
QY 397 TTAATGAAAGGATATATGAAATGGAAGATGATGCGATGATTTGATTTGATTTAATG 456
DB 398 TAAATGAAAGGATATATGAAATGGAAGATGATGCGATGATTTGATTTGATTTAATG 657
QY 447 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 516
DB 448 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 717
QY 517 AAAAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 576
DB 518 AAAAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 777
QY 577 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 636
DB 578 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 837
QY 637 GAAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 696
DB 638 GAAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 897
QY 697 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 756
DB 698 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 957
QY 777 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 816
DB 778 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1017
QY 817 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 876
DB 818 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1077
QY 877 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 936
DB 878 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1137
QY 937 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 996
DB 938 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1197
QY 997 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1056
DB 998 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1257
QY 1057 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1116
DB 1058 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1317
QY 1117 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1176
DB 1118 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1377
QY 1177 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1236
DB 1178 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1437
QY 1237 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1296
DB 1238 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1497
QY 1297 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1356
DB 1298 AATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1557

QY 1357 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1416
DB 1358 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1617
QY 1417 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1476
DB 1418 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1677
QY 1477 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1536
DB 1478 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1737
QY 1537 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1596
DB 1538 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1797
QY 1597 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1656
DB 1598 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1857
QY 1657 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1716
DB 1658 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1917
QY 1717 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1776
DB 1718 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1977
QY 1777 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1836
DB 1778 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2037
QY 1837 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1896
DB 1838 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2097
QY 1897 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1956
DB 1898 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2157
QY 1957 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2016
DB 1958 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2217
QY 2017 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2076
DB 2018 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2277
QY 2077 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2136
DB 2078 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2337
QY 2137 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2196
DB 2138 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2397
QY 2197 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2256
DB 2198 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2457
QY 2257 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2316
DB 2258 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2517
QY 2317 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2276
DB 2318 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2577
QY 2377 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2436
DB 2378 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2637
QY 2437 GATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2496

[illegible]


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612 TrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetMetArgAspArgHisGln 631
613 TGGAGCCCTTTTCAGCAGACACCTGGAGCAATGAGTATGAATCATATGAGNACAGAGATTTTC 632
2179 TGGAGCCCTTTTCAGCAGACACCTGGAGCAATGAGTATGAATCATATGAGNACAGAGATTTTC 2248
2180 TGGAGCCCTTTTCAGCAGACACCTGGAGCAATGAGTATGAATCATATGAGNACAGAGATTTTC 2249
642 AspGlnIleMetMetCysSerMetTyrGlyIleCysValValLysAspGlnLeuAspLeu 651
643 TGGAGCCCTTTTCAGCAGACACCTGGAGCAATGAGTATGAATCATATGAGNACAGAGATTTTC 652
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2240 CACCAAAATATGATGATGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 2299
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713 TGGAGCCCTTTTCAGCAGACACCTGGAGCAATGAGTATGAATCATATGAGNACAGAGATTTTC 732
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2539 GGAGGGAGACATCTATATTTTCAGGCTGAAAGATGCTATATATAAATTTTCAAAATTTTCA 2598
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2780 GGAACAGATGAGACAGATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2839
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2899 CATACCTGCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2922

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RESULT 9

AAV58440

ID AAV58440 standard; DNA; 3555 bp.

XX AC

XX AAV58440;

XX AC

XX 02-DEC-1998 (first entry)

XX DT

XX Modified retinoblastoma tumour suppressor gene.

XX DE

XX Modified retinoblastoma tumour suppressor; RSP protein; cancer therapy;

XX cellular proliferation inhibitor; ss.

XX OS

XX Homo sapiens.

XX XX

XX Key Location/Qualities

XX CDS 7..2793

XX /*tag= a

XX FT

XX W09847091-A2.

XX PN

XX XX


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491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999

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Db 2707 CTGGCAGAAATGACTTCTACTGAAACACGAATGCAAAAATGAAATGATAGATG 2766
G 852 ASDThrSerAsnLysGluGluLys 859
Db 2767 GATACCTCAACCAAGGAAGAGAAA 2790
RESULT 10
AAV54990
ID AAV54990 standard; DNA: 4555 BP.
AC AAV54990;
XX 26-NOV-1998 (first entry)
XX DNA sequence of the specification.
XX Minimal promoter; tetracycline responsive expression vector; TREV;
XX transcriptional transactivation domain; TTD;
XX tetracycline repressor protein; TRP; tetracycline operator;
XX production, stable cell line, protein production;
XX tumour suppressor protein; treatment; cancer; ss.
XX Unidentified.
XX Key Location/Qualifiers
XX 7..2793
XX /*tag- a
XX WO9847185-A2.
XX 27-AUG-1998.
XX 19-FEB-1998; 98WO-US03092.
XX 20-FEB-1997; 97US-0038755.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Hu S, Logothetis CJ, Xu H, Zhou Y;
XX WPI: 1998-480796/41.
XX P-PSDB; AAW71354.
XX New tetracycline responsive expression vectors used for the
XX tightly controlled expression of genes, such as tumour suppressor
XX genes for treating cancers
XX Disclosure: Pages 145-150; 199pp; English.
XX the present sequence appears in the specification, which describes a
XX tetracycline responsive expression vector (TREV), which contains a
XX sequence encoding a fusion protein comprising a transcriptional
XX transactivation domain (TTD) operatively attached to a tetracycline
XX repressor protein (TRP), the first sequence operatively positioned
XX downstream of a promoter. The vector also contains a cloning site
XX operatively positioned downstream of a basal promoter comprising a
XX tetracycline operator. The TREVs can be used to produce stable cell
XX lines in which gene expression is tightly regulated by tetracycline.
XX They can be used for the production of proteins such as tumour
XX suppressor proteins which can be used for treating diseases characterised
XX by abnormal cellular proliferation, particularly cancers.
XX Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T; 0 other;
Alignment Scores:
Pred. No.: 0 Length: 4555
Score: 4401.50 Matches: 858
Percent Similarity: 92.45% Conserved: 0
Best Local Similarity: 92.45% Mismatches: 1
Query Match: 98.84% Indels: 69
DB: 19 Gaps: 1

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 1758 AACTTTCACAAAGATATGATTTTACAAAGATGATCGAAAGATTTTACAAAGATGATCGAAAG 1817
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 512 GlyProThrAspHisLeuGlnSerAlaCysProLeuAsnValProLeuGlnAsnHis 531
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 532 ThrAlaAlaAspMetLeuSerProValAlaCysSerProLysLysLysGlySerThrThr 551
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 552 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 571
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 2658 ACTGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2717


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454 TyrGluGluValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArg 271
DB 1098 TAGAAGAAATTTATCTTTAAATTAAGATCTAGATGCAAGATTATTTTGGATCATGAT 1157
456 LysThrLeuGluThrAspSerLysAspSerPheGluThrGlnArgThrProArgLysSer 291
DB 1158 AAAACCTTCACACATCTCTATACACAGTTTGAACACACAGAACACCAAGAAAGT 1217
458 AsnLeuAspGluValAsnValThrProPheHisThrProValArgThrValMetAsn 311
DB 1218 AATCTTCATCAACAGAGGAGAACTAAATCTCTCCACACATCCAGTTAGACATCTTATCAAC 1277
460 ThrLeuGluGluMetMetMetMetMetMetMetMetMetMetMetMetMetMetMet 331
DB 1278 AATATGACAACTAATATGATGATTTTAAATTCAGCAAGTATCAACCTTCAGAAATCTG 1337
462 ThrSerLysPheAsnAsnCysThrValAsnProLysGluSerLysLeuLysArgValLys 351
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DB 1878 GAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1937
482 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysLysLysLysLys 551
DB 1938 AATTCAGAACAGAAAGATGAACATTTAGAACAGATGAGCAATCGAATCATGGAATCC 1997
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DB 1998 CTTGATGATCTTCATCAATTCATTTATTTGATCTTATTAACAAATCAAAAGCAAGGAA 2057
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488 ArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisLeuLeu 611

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DB 2178 TGCACCTTTTCTAGCAATATATATATATATATATATATATATATATATATATATATATAT 2247
492 AspGluIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 651
DB 2248 GACCAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2297
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DB 2718 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2777
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DB 2778 GATTCAGATCAACAGCAGATGGAAGTAAACATCTCCACAGAGAGATGCAAAATTTTCAAT 2837
512 LeuAlaGluMetThrSerThrArgThrArgMetGluLysGluLysMetAspAspSerMet 851
DB 2838 CTGATGAGAAATATCTTCTACTGGAACAGGATGCAAAAGCAAAATGATGATGATGATG 2897
514 AspThrSerAsnLysGluGluLys 859
DB 2898 CATACCTCAAAATGAGGAGAGAGAA 2921
RESULT 14
AAV58452
ID AAV58452 standard; DNA; 3554 bp.
XX
AC AAV58452;
XX
DT 02-DEC-1998 (first entry)
XX
DE Modified retinoblastoma tumour suppressor gene.
XX
KW Modified retinoblastoma tumour suppressor; RPS protein; cancer therapy;
XX cellular proliferation inhibitor; ss.
XX
QS Homo sapiens.
XX
FH Key 7..2793
FT CDS /*taq- a

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[illegible]

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Db 1667 GTTAAATTTAAAGAGCTTGGATTTTACAAAGTGTATCGAAGAACTTTTATCAAAAGCAGAAGGC 1626
QY 491 AsnLeuThrArgGluMetIleCysHisLeuArgCysGluHisArgIleMetGluSer 491
Db 1627 AACCTGACAAAGAAATGATTAAGAAATTTAGAGGATGATGAGAAACAGCAAGCAAGCAATCC 1686
QY 511 LeuAlaThrLeuSerAspSerProLeuPheAspLeuIleLysGluSerLysAspArgGlu 511
Db 1647 CTTGCAAGGCTCTGCAATTCAGCTTTATTCAGATCTATTAACAAATCAAAAGCAGCAGAA 1746
QY 531 GlyProThrAspHisLeuGluSerAlaCysProLeuAsuLeuProLeuGluInAsuAsnHis 531
Db 1747 GAGCAAAATGATTAATTTCAATTCCTTCTGCTGTAAGATCTCCAAAGAAAAGGTTCAACTACG 1806
QY 551 ThrAlaAlaAspMetLysLeuSerProValArgSerProLysLysLysCysLysSerThrThr 551
Db 1807 ACTGAGAGAGATATGATCTTCTGCTGTAAGATCTCCAAAGAAAAGGTTCAACTACG 1866
QY 571 ArgValAsnSerThrAlaAsuAlaGluThrGlnAlaThrSerAlaPheGlnThrGluLys 571
Db 1867 CGGTAAGAAATCTGCTTCTGCTGTAAGATCTCCAAAGAAAAGGTTCAACTACG 1926
QY 591 ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaIleTyrLeu 591
Db 1927 GCAATGAAATCTGCTTCTGCTGTAAGATCTCCAAAGAAAAGGTTCAACTACG 1986
QY 611 ArgGluAsnThrLeuCysGluArgGluSerGluHisProGluGluGluHisIleIle 611
Db 1987 GCAATGAAATCTGCTTCTGCTGTAAGATCTCCAAAGAAAAGGTTCAACTACG 2046
QY 631 TrpThrLeuPheGluHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 631
Db 2047 GCAATGAAATCTGCTTCTGCTGTAAGATCTCCAAAGAAAAGGTTCAACTACG 2106
QY 651 AspGlnIleMetLeuCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 651
Db 2107 GCAATGAAATCTGCTTCTGCTGTAAGATCTCCAAAGAAAAGGTTCAACTACG 2166
QY 671 PheTyrIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLys 671
Db 2167 TTTCAAAATTAATGTAACATTAATGTAACATTAATGTAACATTAATGTAACATTAATGTAAC 2226
QY 691 ArgValLeuIleLysGluSerMetTyrAspSerIleIleValPheTyrAsnSerValPhe 691
Db 2227 CGTGTGTTGATGAAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2286
QY 711 MetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSer 711
Db 2287 ATGAGAGATTAAGAAATTAATGTAACATTAATGTAACATTAATGTAACATTAATGTAAC 2346
QY 731 ProIleProHisIleProArgSerProTyrLysPheProSerProLeuArgIlePro 731
Db 2347 GCAATGAAATCTGCTTCTGCTGTAAGATCTCCAAAGAAAAGGTTCAACTACG 2406
QY 751 GlyGlyAsuIleTyrLeuSerProLeuLysSerProTyrLysIleSerGlyGlyLeuPro 751
Db 2407 GCAATGAAATCTGCTTCTGCTGTAAGATCTCCAAAGAAAAGGTTCAACTACG 2466
QY 771 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGly 771
Db 2467 AATGAAATTAATGTAACATTAATGTAACATTAATGTAACATTAATGTAACATTAATGTAAC 2526
QY 791 ThrSerGlyGlyGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLys 791
Db 2527 AATGAAATTAATGTAACATTAATGTAACATTAATGTAACATTAATGTAACATTAATGTAAC 2586
QY 811 ArgSerAlaIleLysSerAspProProLysProLeuLysLysIleArgPheAspIleGlu 811
Db 2587 AATGAAATTAATGTAACATTAATGTAACATTAATGTAACATTAATGTAACATTAATGTAAC 2646
QY 831 GlySerAspGluAlaAspLysSerIleHisLeuProLysGluSerTyrPheGlnLys 831

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Db 2647 GATTCAGATGAAGACATGCAATTAATATCTCCACAGAGAGTCAAAATTTTCACGAGAA 2706
QY 832 LeuAlaGluMetThrSerThrArgIleThrArgMetGlnLysMetAsnAspSerMet 831
Db 2707 CTTGCAAGGCTCTGCAATTCAGCTTTATTCAGATCTATTAACAAATCAAAAGCAGCAGAA 2766
QY 852 AspThrSerAsnLysLysGluGluLys 859
Db 2767 GATACCTCAACACAGCAGACAGAAA 2790
RESULT 15
AAQ90059
ID AAQ90059 standard; DNA; 2995 bp.
XX AAQ90059;
AC AAQ90059;
XX 28-NOV-1995 (first entry)
XX Retinoblastoma tumour suppressor gene.
XX Recombinant; adenovirus, expression vector, 130; small lung cancer;
KW hepatocarcinoma; melanoma; retinoblastoma; sarcoma; sickle cell;
KW anemia; Tay-Sachs disease; ss.
XX Homo sapiens.
XX OS
XX FH Key location/Qualifiers
XX FT CDS 139..2925
XX FT /*tag= a
XX PN W09511984-A.
XX PN 04-MAY-1995.
XX PP 25-OCT-1994; 94WO-US12235.
XX PR 19-MAY-1994; 94US-0246007.
XX PR 25-OCT-1994; 94US-0142559.
XX PA (CANJ-) CANJ INC.
XX PI Gregory RJ, Maneval DC, Wills KN;
XX WP1: 1995-178876/23.
XX P-PSDB; AAR74271.
XX PT Adenoviral vector with deletion of viral protein IX contains
XX foreign gene esp. encoding tumour suppressor protein for gene
XX therapy of tumours, reduces contamination by wild type adenovirus
XX disclosure; Fig 3; 92pp; English.
XX The sequence is that of the DNA sequence encoding a retinoblastoma
XX tumour protein. The gene can be used in a novel method involving a
XX recombinant adenovirus expression vector to treat diseases
XX associated with the absence of the 130 of the presence of a mutated
XX 130, e.g. many forms of carcinoma, sickle cell anemia or Tay-Sachs
XX disease.
XX See also AAQ90060-5.
XX SQ Sequence 2995 bp; 975 A; 617 C; 594 G; 809 T; 0 other;
Alignment Scores:
Pred. No.: 0 Length: 2995
Score: 4397.50 Matches: 857
Percent Similarity: 92.4% Gaps: 1
Best Local Similarity: 92.35% Mismatches: 1
Query Match: 98.75% Indels: 69
DB: 16 Gaps: 1
US-09-026-459a-43 (1-859) v AAQ90059 (1-2995)
QY 1 MetProProLysThrProArgLysThrAlaIleThrAlaAlaAlaAlaGluPro 20

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GenCore version 5.1.3
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Sequence: 1 CAGGCAAGGAGGCTAAAAAC.....AAATGAGGATATATGATAGT 3554

Search method: nucleotide search, using SW model

Run on: January 16, 2003, 15:20:17 : Search time 454.619 seconds
(without alignments)
17541.794 Million cell updates/sec

Database: US 09 026-459a 50

Perfect score: 3554

Sequence: 1 CAGGCAAGGAGGCTAAAAAC.....AAATGAGGATATATGATAGT 3554

Scoring table: IDENTITY_NW

Gapop 10.0, Capext 1.0

Searches: 2185289 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4 (70478)

Maximum hit seq length: 0

Maximum hit seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: NGeneseq 1010021*

Result No.	Score	Match	Length	Hit ID	Description
1	4554	100.0	3554	AAV58452	Modified retinobla
2	4550.8	99.9	3555	AAV58440	Modified retinobla
3	4550.8	99.9	3555	AAV58440	DNA sequence of th
4	4549.8	99.9	4849	AAZ29391	Human retinoblasto
5	4549.8	99.9	4849	AAZ29391	Human androgen rec
6	4549.8	99.9	4849	AAZ29391	breast cancer rela
7	4520.2	99.0	4597	AAZ70536	Human retinoblasto
8	4520.2	99.0	4597	AAZ70536	Human retinoblasto
9	4518.6	99.0	4597	AAZ1369	Human retinoblasto

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	Hit ID	Description
1	4554	100.0	3554	AAV58452	Modified retinobla
2	4550.8	99.9	3555	AAV58440	Modified retinobla
3	4550.8	99.9	3555	AAV58440	DNA sequence of th
4	4549.8	99.9	4849	AAZ29391	Human retinoblasto
5	4549.8	99.9	4849	AAZ29391	Human androgen rec
6	4549.8	99.9	4849	AAZ29391	breast cancer rela
7	4520.2	99.0	4597	AAZ70536	Human retinoblasto
8	4520.2	99.0	4597	AAZ70536	Human retinoblasto
9	4518.6	99.0	4597	AAZ1369	Human retinoblasto

10	3515.6	98.9	4740	24	AHK86079	Human retinoblasto
11	3451.6	97.1	4579	9	AAAH1261	probe for retinobl
12	3443.8	96.9	3455	19	AAV58441	Modified retinobla
13	3379.8	95.1	3392	19	AAV58442	Modified retinobla
14	3351.6	94.3	3461	19	AAV58447	Modified retinobla
15	3311.6	93.2	3323	19	AAV58443	Modified retinobla
16	3253.8	91.6	3266	19	AAV58444	Modified retinobla
17	3222.8	90.7	3323	19	AAV58446	Modified retinobla
18	3212.2	90.4	3218	19	AAV54991	DNA sequence of th
19	3208.2	90.3	3234	15	AAZ72690	retinoblastoma 94k
20	3192.4	89.8	3383	19	AAV58451	Modified retinobla
21	3180.4	89.5	3377	19	AAV58450	Modified retinobla
22	3126.8	88.0	3347	19	AAV58448	Modified retinobla
23	3107.8	87.4	3113	19	AAV58445	Modified retinobla
24	3009.4	84.7	5056	10	AAV90489	cDNA of human reti
25	2857.8	80.4	2994	19	AAV40004	retinoblastoma pro
26	2856.2	80.4	2994	14	AAV41545	retinoblastoma pro
27	2856.2	80.4	2994	21	AAZ13287	Wild type human re
28	2854.8	80.3	2995	20	AAV90450	Human p110-Rb ret
29	2854.8	80.3	2995	22	AAH25755	retinoblastoma tum
30	2854.8	80.3	2995	22	AAH25755	retinoblastoma tum
31	2854.8	80.3	2995	23	AAH25755	retinoblastoma tum
32	2854.8	80.3	2994	11	AAV904713	Cancer suppressor
33	2853.2	80.3	2995	16	AAV90059	retinoblastoma tum
34	2851.6	80.2	2995	29	AAZ03737	cDNA encoding a re
35	2848.4	80.1	2995	16	AAV58449	Human Rb10 cDNA
36	2827.4	79.6	3161	19	AAV58449	Modified retinobla
37	835	23.5	18303	20	AAV904502	Human retinoblasto
38	841.8	23.4	18177	10	AAV90490	DNA of human retin
39	220.8	6.2	1598	18	AAZ62493	Anti-ssense suppress
40	220.8	6.2	1598	18	AAZ62493	Direct tandem repe
41	220.8	6.2	1598	18	AAZ62493	Construct pRR1-2A
42	220.8	6.2	1598	18	AAZ62493	Construct pRR1-2A
43	220.8	6.2	1598	18	AAZ62493	Construct pRR1-2A
44	220.8	6.2	1598	18	AAZ62493	Construct pRR1-2A
45	220.8	6.2	1598	18	AAZ62493	Construct pRR1-2A
46	220.8	6.2	1598	18	AAZ62493	Construct pRR1-2A
47	220.8	6.2	1598	18	AAZ62493	Construct pRR1-2A
48	220.8	6.2	1598	18	AAZ62493	Construct pRR1-2A
49	220.8	6.2	1598	18	AAZ62493	Construct pRR1-2A
50	220.8	6.2	1598	18	AAZ62493	Construct pRR1-2A

ALIGNMENTS

RESULTS

AAV58452 standard: DNA: 4554 bp.

AAV58452:

82 bp 1998 (first entry)

Modified retinoblastoma tumour suppressor gene.

Modified retinoblastoma tumour suppressor gene. FSP p110-Rb. Cancer therapy.
retinoblastoma inhibitor, ss.

Homo sapiens.

Key Location/Qualifiers

CDS 7..2793

/*aaq. a

W09837091-A2.

27-AUG-1998.

19-FEB-1998; 98W0-0504041.

20-FEB-1997; 97US-0048118.

(BAYU) BAYLOR COLLEGE MEDICINE.

(TEXA) UNIV TEXAS SYSTEM.

Reedict WF, Hu S, Xu B, Zhou Y;

2 FEB-1997; 97US-0038755.
 XX CEXA J UN-V TEXAS SYSTEM.
 XX Hu S. Logothetis CJ, Xu H, Zhou Y;
 XX Wilt 1998-480796/41.
 XX P ENR: AAW7,454.
 XX
 XX This tetracycline responsive expression vector, used for the
 XX tightly controlled expression of genes, such as tumour suppressor
 XX genes for treating cancers
 XX
 XX Description: Pages 145-150; 190pp; English.
 XX
 XX The present sequence appears in the specification, which describes a
 XX tetracycline responsive expression vector (TREV), which contains a
 XX sequence encoding a fusion protein comprising a transcriptional
 XX transactivation domain (TAD) operatively attached to a tetracycline
 XX repressor protein (TRP), the first sequence operatively positioned
 XX downstream of a promoter, the vector also contains a cloning site
 XX operatively positioned downstream of a basal promoter comprising a
 XX tetracycline operator, the TRPVs can be used to produce stable cell
 XX lines in which gene expression is tightly regulated by tetracycline.
 XX They can be used for the production of proteins such as tumour
 XX suppressor proteins which can be used for treating diseases characterised
 XX by abnormal cellular proliferation, particularly cancers.
 XX
 XX Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T; 0 other;

Query: Match 99.9%; Score 3550.8; DB 19; Length 3555;
 Best local Similarity 99.9%; Pred. No. 0;
 Matches 3552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 601 TTATTAGCTAAAGGCAAGTATTAAATGGAATATATCTGTGATTCATTCAGTAA 663
 DB 601 TTATTAGCTAAAGGCAAGTATTAAATGGAATATATCTGTGATTCATTCAGTAA 660
 QY 661 ATGCTAATGAGTCTTGAATTTTATTAAAGTCTGAGTCTGATGCTGAGTAAAT 723
 DB 661 ATGCTAATGAGTCTTGAATTTTATTAAAGTCTGAGTCTGATGCTGAGTAAAT 720
 QY 721 TAAATAATGCTTATATACCAATTAATCTTCAATGCTGAGTCTGAGTAAAT 780
 DB 721 TAAATAATGCTTATATACCAATTAATCTTCAATGCTGAGTCTGAGTAAAT 780
 QY 781 AGAGTGTAAAGTATGCAAAATTAATAGAAATATATGAGTCTGATTCAGTAA 843
 DB 781 AGAGTGTAAAGTATGCAAAATTAATAGAAATATATGAGTCTGATTCAGTAA 840
 QY 841 AAGAAATGATGATTAATATAGATGAGTGTGAGTAAATGTTTATTCAAAATTTTATAGCT 900
 DB 841 AAGAAATGATGATTAATATAGATGAGTGTGAGTAAATGTTTATTCAAAATTTTATAGCT 900
 QY 901 TTTAAGAAATGCTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 963
 DB 901 TTTAAGAAATGCTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 960
 QY 961 AAGGATATGAGTAAATTTTATTAAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1020
 DB 961 AAGGATATGAGTAAATTTTATTAAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1020
 QY 1021 CATGATTAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1080
 DB 1021 CATGATTAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1080
 QY 1081 AAAAGTAAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1140
 DB 1081 AAAAGTAAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1140
 QY 1141 ATGACATGATGCAATTAATTAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1200
 DB 1141 ATGACATGATGCAATTAATTAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1200
 QY 1201 AATGCTAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1260
 DB 1201 AATGCTAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1260
 QY 1261 GTGAGGATATAGATACATCTTTAAGAGAAATTTGCTAAGTCTGAGTCTGAGTCTGAGTCT 1320
 DB 1261 GTGAGGATATAGATACATCTTTAAGAGAAATTTGCTAAGTCTGAGTCTGAGTCTGAGTCT 1320
 QY 1321 GTGAGGATATAGATACATCTTTAAGAGAAATTTGCTAAGTCTGAGTCTGAGTCTGAGTCT 1380
 DB 1321 GTGAGGATATAGATACATCTTTAAGAGAAATTTGCTAAGTCTGAGTCTGAGTCTGAGTCT 1380
 QY 1381 TGTGCTAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1440
 DB 1381 TGTGCTAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1440
 QY 1441 GACAGATTTTCAATATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1500
 DB 1441 GACAGATTTTCAATATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1500
 QY 1501 AATGCTAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1560
 DB 1501 AATGCTAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1560
 QY 1561 AATGCTAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1620
 DB 1561 AATGCTAATGCTTCAAGTCTGATTCATAGACAGTCTTCAAGTCTGATTCATAGACAG 1620
 QY 1621 GAAGGATATAGATACATCTTTAAGAGAAATTTGCTAAGTCTGAGTCTGAGTCTGAGTCT 1680
 DB 1621 GAAGGATATAGATACATCTTTAAGAGAAATTTGCTAAGTCTGAGTCTGAGTCTGAGTCT 1680

Qy	182	CATTATGTCACAAATTAAAGCATACCAATCATCTGACAGACAGACAGTTCAGTTAACTTGSS	241
Db	313	CATTATGTCACAAATTAAAGCATACCAATCATCTGACAGACAGACAGTTCAGTTAACTTGSS	472
Qy	242	ACAAACCTTCATCTGTCGATCGAGCTATCGGGAGCTTTATATCTCAACACAAAAAGAACTG	301
Db	314	ACAAACCTTCATCTGTCGATCGAGCTATCGGGAGCTTTATATCTCAACACAAAAAGAACTG	473
Db	373	AGAAAGTTTATCTGTGATGAGATATCTGAGATTTATATTTAAAGAAATTAAGAACTT	472
Qy	302	GGGCAATCTGATCTTTATTCGACGACCTTCACGTAGTGTGATGATGATGCTTCATTTACG	361
Db	433	GCGCAATCTGATCTTTATTCGACGACCTTCACGTAGTGTGATGATGATGCTTCATTTACG	492
Qy	362	AGCTACAGAAATATAGAAATCAGTGTGATTAATTTCTTTACTTATTAAGAAATATG	421
Db	493	AGCTACAGAAATATAGAAATCAGTGTGATTAATTTCTTTACTTATTAAGAAATATG	552
Qy	422	ATACCACTACCAAGTTGATTAAGCTATCTCAACATCTGTGAGGAAGATGATGATGATG	481
Db	553	ATATATATATTAAGTTGATTAAGCTATCTCAACATCTGTGAGGAAGATGATGATGATG	611
Qy	492	TTTCACCTCTTCACCAATTTGCGAAGGACATGTGAGCTTATATATTTGACATCAACCAACA	541
Db	613	TTTCACCTCTTCACCAATTTGCGAAGGACATGTGAGCTTATATATTTGACATCAACCAACA	672
Qy	542	CTTCTATATATATTAAGATTAATTTCTGATTTGAGTGTGAAAGTCTGTGATTCATATTT	601
Db	673	CTTCTATATATATTAAGATTAATTTCTGATTTGAGTGTGAAAGTCTGTGATTCATATTT	732
Qy	602	TATTTAGCTAAAGGCGGAGTATTACAAATCGACATCATCTGGTGGATTTGATTTGATTA	661
Db	733	TATTTAGCTAAAGGCGGAGTATTACAAATCGACATCATCTGGTGGATTTGATTTGATTA	792
Qy	662	AGCTATGCTGCTTGACATATTTATTAACCTCTCACCTCCCATCTGCTCAACGAATCTA	721
Db	793	AGCTATGCTGCTTGACATATTTATTAACCTCTCACCTCCCATCTGCTCAACGAATCTA	852
Qy	722	ATAAATATATCTATATATTAATTTCTGATTTGAGTGTGAAAGTCTGTGATTCATATTT	781
Db	853	ATAAATATATCTATATATTAATTTCTGATTTGAGTGTGAAAGTCTGTGATTCATATTT	912
Qy	782	GGATCTCCACCGATAGCAAAAACACTAATAATGATACAGATCACTGCTGCTGCTGCTG	841
Db	913	GGATCTCCACCGATAGCAAAAACACTAATAATGATACAGATCACTGCTGCTGCTGCTG	972
Qy	842	AAGCAATGATGCTTAATATAGATTCAGCTCGAAGAAATGCTTTATTTTCAAAAATTTAT	901
Db	973	AAGCAATGATGCTTAATATAGATTCAGCTCGAAGAAATGCTTTATTTTCAAAAATTTAT	1033
Qy	902	TTATGATTTCTCTGTGATTTGTTATACATCTAAATGAGATCTGAGTGTGAAATCTTTCTA	961
Db	1033	TTATGATTTCTCTGTGATTTGTTATACATCTAAATGAGATCTGAGTGTGAAATCTTTCTA	1092
Qy	962	AACCATACCAAGAAATTTATCTTTAAATTAAGCAATCTAGATCGAATATCTTGGATCT	1021
Db	1093	AACCATACCAAGAAATTTATCTTTAAATTAAGCAATCTAGATCGAATATCTTGGATCT	1152
Qy	1022	ATGATAAAATCTTTGACATCTGATCTATACAGATTTTGAACACACAGACATCACTACAA	1081
Db	1153	ATGATAAAATCTTTGACATCTGATCTATACAGATTTTGAACACACAGACATCACTACAA	1212
Qy	1082	AAAGTAACCTTGATGAGAGATGTAATTTGCTGTACATCTGATTAAGTCTGTTA	1141
Db	1213	AAAGTAACCTTGATGAGAGATGTAATTTGCTGTACATCTGATTAAGTCTGTTA	1272
Qy	1142	TGAACATATCCCAACAAATTAAGAIGATTTTAAATTCACCAAGTATCAACCTTCACAGAA	1201
Db	1273	TGAACATATCCCAACAAATTAAGAIGATTTTAAATTCACCAAGTATCAACCTTCACAGAA	1333
Qy	1202	ATCTGATTTGCTATTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATG	1261
Db	1333	ATCTGATTTGCTATTTTAACTGATGATGATGATGATGATGATGATGATGATGATG	1393
Qy	1262	TGAACATATATATATATATTTTAAATTAAGATTTTAAATTCACCAAGTATCAACCTTC	1272

[illegible][illegible]


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11 2469 GATACAGTCIGGATTCATGTCCTCAAGAGATGACAGTAAATTTTCCAGAGGCTG 2648
12 2470 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 2939
13 2471 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 2708
14 2472 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 2999
15 2473 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 2768
16 2474 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3059
17 2475 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 2828
18 2476 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3119
19 2477 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 2888
20 2478 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3179
21 2479 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 2948
22 2480 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3239
23 2481 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3008
24 2482 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3299
25 2483 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3068
26 2484 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3359
27 2485 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3128
28 2486 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3419
29 2487 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3188
30 2488 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3479
31 2489 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3248
32 2490 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3539
33 2491 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3308
34 2492 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3554
35 2493 TTTAATGCTTACATTTTAAATGCTTCAAGCTGCTTGGGATATATAAATGCTGAGATGCTGAAT 3323
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Search completed: January 16, 2003, 23:41:50
Job time : 477.519 secs


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QY 332 LeuPheLeuAspHisAspHisThrLeuGlnThrAspSerIleAspSerPheGluThrGln 321
DB 1141 TTAATTTTGATCATGATGATAAAGGCTTCACAGTATTCATAGACACATTTTGGAAACAG 1200
QY 422 ArgThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPro 341
DB 1201 AGAACACACACCAAAAGCTAACTCTGATCAAGAGGCTGAATGTAATTCCTCCACACATCCA 1260
QY 442 ValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAsp 361
DB 1261 GTTAGGACCTGTTATGACACTATCTAACAAATTAATGATGATTTTAAATTCAGCAACTGAT 1320
QY 662 GlnProSerGluAsnLeuIleSerTyrPheAsnAspCysThrValAsnProLysGluSer 381
DB 1421 CAAGCTTCAGAAATCTGATTCCTATTTTAAACAGTGCACAGTGAATCCAAAGAAAGT 1380
QY 662 IledLysArgValLysAspIleCysTyrIlePheLysCysLysPheAlaLysAlaVal 401
DB 1461 ATAGTGAAGAGAGTGAAGAGATATAGGATACATCTTTAAAGAGAAAATTTCCTAAAGCTGTG 1440
QY 422 GlyIleLysValGluIleLysSerGlnArgTyrLysLeuGlyValArgLeuTyrTyr 421
DB 1441 GCACAGGGTGTGTCGAAATTTGATACACAGGATACAAACTTCGAGTTCCTTGTATATAC 1500
QY 442 ArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSer 441
DB 1461 AGATGAATGGAATCATGCTTAATATAGAAAGAGATGATTATCTTCAAAATTTTATAGC 1560
QY 442 LysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuLeuAlaCysAlaLeuGluVal 461
DB 1561 AAATCTGCGAATGACAACTATTTTATATGCTTTTATGCTTTTATGCTTTTATGCTTTTATG 1620
QY 462 MetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPhe 481
DB 1621 ATGCCACATATAGCAGAGTACATCTCAGAACTTCATCTTCGGAACACATTTGCTCTTC 1680
QY 442 ProThrPheLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSer 501
DB 1641 CATATGATTCGATGCTGCTTAATTTTAAAGCTTTTATGATTTTATGATTTTATGATTTTAT 1740
QY 662 PheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGlu 521
DB 1741 TTTATCAAAAGCAGAGGCACTTCACAAAGACAAATGATCAAAACATTTTACAGCACTCAA 1800
QY 622 HisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuLys 541
DB 1801 CATGGAATATAGCAATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCAT 1860
QY 642 GlnSerLysAspArgGluGlyThrThrAspHisLeuGluSerAlaCysProLeuAsnLeu 561
DB 1861 TAAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 662 ProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLys 581
DB 1921 GCTCTCAGAAATAATCAGACATGAGGAGATAGTATCTTCTCTCTCTCTCTCTCTCTCTCT 1980
QY 662 LysLysLysSerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSer 601
DB 1981 AAAAAGGCTTCAAGTACGGGCTGAAATTTTACATGCAAAATGACACACACACACACACAC 2040
QY 662 AlaPheLeuThrGlnLysPheLysSerThrSerLeuSerLeuPheLysVal 621
DB 2041 GCTCTCAGAAATAATCAGACATGAGGAGATAGTATCTTCTCTCTCTCTCTCTCTCTCTCT 2100
QY 622 TyrArgLeuAlaTyrLeuArgLeuAsnThrLeuGluGluArgLeuSerGluHisPro 641
DB 2101 TATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
QY 642 GlnLeuLysHisIleIleTyrThrLeuPheGluHisThrLeuGluAsnGluTyrGluLeu 661
DB 2161 GAAATAGAAATATATATATATATATATATATATATATATATATATATATATATATATATAT 2220

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QY 662 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVal 681
DB 2221 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
QY 682 LysAsnIleAspLeuLysPheLysIleValThrAlaTyrLysAspLeuProHisAla 701
DB 2281 AACAAATATAGACCTTAAATTTCAAAATCATTTGAACAGCATACAAAGCACTTCCTCAATCT 2340
QY 702 ValGlnGluThrPheLysArgValIleLysGluIleLysGluIleLysSerIleLeuVal 721
DB 2341 GTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
QY 722 PheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThr 741
DB 2401 TCTATAACTGAGCTTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
QY 742 ArgProThrLeuSerProIleProHisIleProValSerProTyrLysPheProSer 761
DB 2461 AGGCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
QY 762 SerProLeuArgIleProGlyLysAsnIleTyrIleSerProLeuLysSerProTyrLys 781
DB 2521 TCACTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
QY 782 IleSerGluGlyLeuProThrProThrTyrMetThrProArgSerArgIleLeuValSer 801
DB 2581 ATTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640
QY 802 IleGlyLysSerPheThrSerGlyLysPheGluLysIleAsnGluMetValTyrAsn 821
DB 2641 ATTGCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
QY 822 SerAspArgValLeuLysArgSerAlaGluGlySerAsnProProLysProLysLys 841
DB 2701 AGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
QY 842 LeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGlu 861
DB 2761 CTACGCTTTTATATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
QY 862 SerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgMetGluLysGln 881
DB 2821 TCCAAATTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
QY 882 LysMetAsnAspSerMetAspThrSerAspLysGluGlyLys 895
DB 2881 AAAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2920

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RESULT 4

AAV40004

ID AAV40004 standard; DNA; 2994 BP.

XX AAV40004;

AC AAV40004;

XX 15-FEB-1999 (first entry)

XX Retinoblastoma protein RB.

DE Retinoblastoma protein RB.

XX Retinoblastoma protein RB; E2F; transcription factor; human;

KW Bladder cancer; rhabdomyosarcoma; angiosarcoma; diabetic retinopathy;

KW thyroid hyperplasia; Graves' disease; psoriasis;

KW benign prostatic hyperplasia; thymoma; thymic carcinoma;

KW peripheral vascular disease; therapy; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key location/Qualifiers

FH 149..2925

FT /*aa- a

XX

XX W09821228-A1.

XX

XX 22-MAY-1998.

PD


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1081 GCATGGAATTTGAATGGTGTAAATTTAAAAGCCTTTGATTTTACAAAGTGATCAAACT 1740
1082 PheTlePsaIaGluGlyAsnLeuArgGluMetTleLysHisLeuGluArgTyrGlu 521
1083 TTTTATCAAAAGTAAAGTAAATTTGCAAGCAAAATATATAAAATTTAGAACGATGTGAA 1800
1084 HisArgTleMetGluSerLeuAlaIrrLeuSerAspSerProLeuPheAspLeuIleLys 541
1085 CAICGAAATTCAGCAATCCCTGCAATGCTGACATTCACCTTTATTTGATCTTATTA 1860
1086 GluSerTyrAspArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeu 561
1087 TAATCAAAAGTAAAGTAAATTTGCAAGCAAAATATATAAAATTTAGAACGATGTGAA 1920
1088 ProLeuGluAsnAspHisThrAlaAspMetTyrLeuSerProValArgSerProLys 581
1089 CTCTCTCTAGAAATACACACATCTATATATATCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
1090 LysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSer 601
1091 AAAAAAGGTTCAATTAAGGCTGTAATTTCTACTGCAAAATGCACAGACACAAAGCTTCA 2040
1092 AlaGluSerThrGluGlySerThrSerLeuSerSerLeuPheTyrLysVal 621
1093 GCTTCTGACAGCTAAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2100
1094 TyrArgLeuAlaTyrLeuArgGluAsnThrLeuCysGluArgLeuLeuSerGluHisPro 641
1095 TATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 2160
1096 GluLeuGluHisTleTleTleTleTleTleTleTleTleTleTleTleTleTleTleTle 661
1097 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2220
1098 MetAlaPheArgHisGluSerThrMetMetCysSerMetTyrGlyLeuCysGlyVal 681
1099 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
1100 LysAsnHisLeuGlySerThrHisLeuValThrAlaTyrLysAspLeuProHisAla 701
1101 AAGAAATATAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2340
1102 ValLeuSerThrPheLeuArgValLeuLysLeuGluGluTyrAspSerIleIleVal 721
1103 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
1104 PheTyrAspSerValPheMetGluArgGluLysThrAsnLeuLeuGluGluTyrAlaSerThr 741
1105 TTTTATCAAAAGTAAAGTAAATTTGCAAGCAAAATATATAAAATTTAGAACGATGTGAA 2460
1106 ThrLeuSerThrLeuSerThrLeuSerThrHisTyrArgSerProTyrLysThrProSer 761
1107 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
1108 SerProLeuArgGluPheArgGluGluGluGluGluGluGluGluGluGluGluGluGlu 781
1109 TATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 2580
1110 ThrSerThrLeuSerThrLeuSerThrHisTyrArgSerProTyrLysThrProSer 801
1111 ATTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2640
1112 HisGlyLeuSerPheCysThrSerThrGlySerThrAlaGluGluGluGluGluGluGlu 821
1113 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
1114 SerAspArgValLeuLysAspSerAlaGluGluGluGluGluGluGluGluGluGluGlu 841
1115 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760
1116 ThrArgPheAspTleGluGlySerAspThrAlaAspCysSerLysHisLeuProGlyGlu 861
1117 TATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 2820

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007 862 SerLysPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 881
008 2821 TCTAAATTTCTAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2880
009 882 LysMetAspSerMetAspThrSerAspLysGlyLeuLys 895
010 2881 AAATGATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2922

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RESULT 5

AAZ40287 standard; cDNA: 2994 bp.

XX AAZ40287;

AC AAZ40287;

DT 24-FEB-2000 (first entry)

DE Wild type human retinoblastoma gene.

KW RB gene; human; retinoblastoma gene; mutation detection; immunoscreening;

KW retinoblastoma diagnosis; hereditary retinoblastoma; secondary cancer;

KW osteosarcoma; fibrosarcoma; glioblastoma; breast cancer;

KW tumorigenesis suppression; ss.

XX Homo sapiens.

XX US5998134-A.

XX 07-DEC-1999.

XX 07-JUN-1995; 950S-0482627.

XX 15-OCT-1987; 870S-0108748.

XX 28-SEP-1992; 920S-0951947.

XX (RBG) UNIV CALIFORNIA.

XX Lee EYP, Lee W;

XX WPI: 2000-052540/04

XX P-PSDH: AAY55060.

XX Detecting retinoblastoma gene cancer in mammals -

XX Example 6; Fig 7; 34pp; English.

This sequence represents the wild type human retinoblastoma gene. The invention relates to a method of detecting a mutated retinoblastoma (Rb) nucleic acid in mammals comprising hybridizing an isolated full-length, wild-type Rb (wRb) cDNA probe to a cell sample and detecting a mutated Rb nucleic acid. The method is useful as a diagnostic tool for diagnosing retinoblastoma. Rb cDNA or genomic DNA are preferably used as probes to determine the defect region of the Rb gene through genomic DNA blotting analysis or using the method of restriction fragment length polymorphism analysis to determine the diseased allele. Cloned Rb cDNA can be used to generate specific anti-Rb protein (anti-pRB10) antibodies which are useful for immunoscreening of tissue biopsy. The diagnostic method is particularly intended for use in screening families with a history of hereditary retinoblastoma and for screening their children. It may also be used in prophylactic and postnatal screening and for the prediction of the development of secondary cancer, such as, osteosarcoma, fibrosarcoma, glioblastoma, breast cancer, whether or not connected with retinoblastoma. The method is also used in the suppression of tumorigenesis where the absent Rb protein pRB10 will be provided through the molecular induction and gene transplating of the Rb cDNA to the individual in need of pRB10.

SQ Sequence 2994 bp; 974 A; 618 C; 594 G; 808 T; 0 other;

Alignment Scores:

Prod. No.:

Score: 894

Matches: 4609/00

Penalty: 100.00%

Similarity: 0

Length: 2994

Matches: 894

Conservative: 0


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CY 712 VLLHLLSTPFFPCYSATVALEHLELYSLGLGLIHLTYRASESRLPILVAL 721
DB 2441 GLLACAGACATATCAAAAGCTCTTTCATCAACAGACAGATCATCTATTAAGTA 2400
CY 722 PheLYrAsnSerValPheMetGluAspGlnLysThrAsnLeuGlnTyrAlaSerThr 741
DB 2401 TTTATATATGCTGCTTTATATATATATATATATATATATATATATATATAT 2460
CY 742 ArgProThrLeuSerProIleProHisIleProArgSerProIleTyrLysPheProSer 761
DB 2461 AGGAGGATACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2520
CY 762 SerProLeuArgIleProGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 781
DB 2521 TCACTCTTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2580
CY 782 HESORGLGLYLCOPTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 801
DB 2581 ATTTATATATATATATATATATATATATATATATATATATATATATATAT 2640
CY 802 HecLYrAsnSerPheGlyThrSerGlnLysPheClnLysIleAsnGlnMetValCysAsn 821
DB 2641 ATTCTATATATATATATATATATATATATATATATATATATATATATAT 2700
CY 842 SerAspArgValLeuLysArgSerAlaGlnGlySerAsnProProLysProLeuLysLys 841
DB 2701 AGGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2760
CY 862 LeuArgPheAspIleGlnGlySerAspGlnAlaAspGlnSerLysHisLeuProGlyGlu 861
DB 2761 CTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2820
CY 882 SerLysPheGlnGlnLysGlnAlaGlnMetThrSerThrArgThrArgMetClnLysGln 881
DB 2821 TCCAAATCTCAGCAAACTCCGAGAAATGACTTCTACTCTGAAATATGAAATG 2880
CY 882 LysMetAlaAspSerMetAspThrSerAsnLysClnLysLys 895
DB 2881 AAAATGAAATGATATATATATATATATATATATATATATATATATATATAT 2920
P-SDS:
AAAX90450
CY AAAX90450 standard; cDNA, 2995 bp.
CY AAAX90450:
CY AAAX90450:
CY 27 SEP-1999 (first entry)
CY Human p110-RB retinoblastoma tumour suppressor encoding cDNA
CY Human p110-RB; retinoblastoma; tumour suppressor; gene therapy;
CY adenooviral protein IX; recombinant adenovirus expression vector;
CY cell cycle; p53; mitosis; cell death; apoptosis; thymidine kinase;
CY cancer; ss.
CY Homo sapiens.
CY Key Location/Qualifiers
CY COS 139..2925
CY /*tag= a
CY /product= "p110-pp"
CY /note= "retinoblastoma tumour suppressor"
CY 187 452210-A.
CY 188 452210-A.
CY 189 452210-A.
CY 190 452210-A.
CY 191 452210-A.
CY 192 452210-A.
CY 193 452210-A.
CY 194 452210-A.
CY 195 452210-A.
CY 196 452210-A.
CY 197 452210-A.
CY 198 452210-A.
CY 199 452210-A.
CY 200 452210-A.

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XX (CANJ-) CANJII INC.
XX Gregory RJ, Manaval DC, Wills KN;
XX WPI; 1999-443568/37.
XX P-PSDB; AAY24471.
XX Recombinant adenooviral vectors useful for gene therapy of cancer,
XX especially p53 deficient tumours
XX Disclosure; Fig 3; 50pp; English.
XX The present invention describes a composition comprising a recombinant
XX adenoovirus expression vector, where the vector has an insert of
XX exogenous DNA comprising a gene encoding a foreign protein and
XX adenoovirus DNA in which all of the coding sequences of E1a, E1b, and
XX protein IX, and part of E3 are deleted. The vectors are useful in gene
XX therapy treatment of cancer, especially for treating p53 deficient
XX tumours. The vector enables safer and more efficient gene therapy of
XX cancer. The present sequence encodes human p110-RB retinoblastoma
XX tumour suppressor which can be used as the foreign gene in the above
XX vector.
XX Sequence: 2995 bp, 975 A, 618 C, 593 G, 899 T; 0 other;
Alignment Scores:
Pred. No.: 0 Length: 2995
Score: 4609.00 Matches: 894
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 20 Gaps: 0
US-09-026-459a-29 (1-895) x AAAX90350 (1-2995)
CY 2 GlnAspSerGlyProGluAspLeuProLeuValArgLeuGlnPheGlnThrGluGln 21
DB 341 CAGCACAGCGCGCGCGAGGACCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 100
CY 22 ProAspPheThrAlaLeuGlnCysGlnLysClnLysIleProAspHisValArgGluArgAla 41
DB 301 CCTATTTTACTGCTATATGTCAGAAATTAAGATACAGATCATGTCCAGAGAGAGCT 460
CY 42 TrypticThrProGlnLysValSerSerValAspGlyValLeuGlnGlyTyrIleGlnLys 61
DB 361 TGGTAACTTGGCAGAAATTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
CY 62 TrypticThrLeuArgPheGlnLysIleGlnLysIleGlnLysIleGlnLysIleGln 81
DB 421 AAAAAGGAACTTGGGGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
CY 82 PheThrPheThrGlnLeuGlnLysAsnIleGlnIleSerValHisLysPhePheAsnLeu 101
DB 481 TTCACITTTATGAGCTACAGAAACATAGAAATCAGTGTGATATAATCTCTTAACTTA 140
CY 102 LcclLysClnLysAspThrSerThrLysValAspAsnAlaMetSerArgGlnLysLys 121
DB 541 CTAAAGAAATTCATACCAAGTATGATTAATGCTATGATGATGATGATGATGATG 600
CY 122 TyrAspValLeuPheAlaLeuPheSerLysLeuGlnLysIleGlnLysIleGlnLys 141
DB 601 TATCATATATCTTGGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
CY 142 ThrGlnProSerSerSerIleSerThrGlnIleAsnSerAlaLeuValLeuLysValSer 161
DB 661 ACAAAATATATATATATATATATATATATATATATATATATATATATATAT 720
CY 162 TrypticThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGlnAspAspLeuValIle 181
DB 721 TGGATCATATTTTATATAGCTAAAGGGAGGATATACAAATGCAAGATGATCTGCT 780
CY 182 SerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeu 201

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XX AAX00747:
XX 13 APR-1999 (first entry)
XX cDNA encoding a retinoblastoma protein designated pPRB-110 or p110-RB
XX Retinoblastoma protein; RB protein; pPRB-110; p110-RB; inhibition;
XX proliferation; cancer; retinoblastoma, secondary osteosarcoma,
XX breast cancer; small-cell lung cancer; fibrosarcoma; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 139..295
XX /*tag= a
XX /product= RB protein
XX /name= except. (pos: 226..228, aa: Glu)
XX OS8651991-A.
XX XX
XX 22 DEC-1998.
XX XX
XX 13 SEP-1994: 940S-0406513.
XX XX
XX 13 SEP-1994: 940S-0406513.
XX 31 AUG-1997: 870S-0094547.
XX 13 SEP-1997: 870S-00948612.
XX 16 OCT-1997: 870S-0108748.
XX 31 OCT-1998: 880S-0265829.
XX 11 JUL-1990: 900S-0550877.
XX 16 JUL-1990: 900S-0553892.
XX 13 JUL-1990: 900S-0553905.
XX 17 OCT-1991: 910S-0778510.
XX 14 JUL-1992: 920S-0614039.
XX 02 OCT-1992: 920S-0956472.
XX 17 JUN-1993: 930S-0079207.
XX 13 SEP-1993: 930S-0121108.
XX 24 SEP-1993: 930S-0126810.
XX (CAN) ) CAN/J INC.
XX (RBC) ) UNIV CALIFORNIA.
XX Friedrich DW. Johnson D, Lee EY, Lee W, Shepard HM;
XX Wang NP;
XX W017: 1999-080477/07
XX P 850B: AAW67801.
XX Inhibition of cancer cell proliferation - with retinoblastoma
XX protein or polypeptide
XX Example 1: Fig 2A-K; 72pp; English.
XX The present sequence encodes a human retinoblastoma (RB) protein
XX designated pPRB-110 or p110-RB. The protein is used in a method
XX for inhibiting proliferation of pathologically proliferating cells
XX lacking endogenous functional retinoblastoma protein. The method
XX comprises contacting the cells with a polypeptide comprising a 56 kD
XX C-terminal fragment of retinoblastoma protein. The method is useful
XX for treating cancers, especially retinoblastoma or secondary
XX osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
XX Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 2995
XX Score: 4609.00 Matches: 894
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query 895 bp: 59.89% Indels: 0
XX Gaps: 20

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ng-09-026-459a-29 (1-895) x AAX00737 (1-2995)
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DB 241 CAGATACGACCGCCGGAGGACCGCCGCTGCGTCAGCCTTCAGTTTGAGAAATACAGAA 300
QY 22 ProAspPheThrAlaLeuGlyGlnGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGly 41
DB 301 CGGCAATTAAGCAATTAAGTCAGAAATTAAGCAATTAAGCAATTAAGCAATTAAGCA 360
QY 42 TrpLeuThrTrpGlnGlyValSerSerValAspGlyValLeuGlyGlyTrpIleGlnGly 61
DB 361 TGGTTACCTGGAGAAATTTTCATCTGTGATGATGATGATGATGATGATGATGATGAT 420
QY 62 GysGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 81
DB 421 AAAAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAAT 480
QY 82 PheThrPheThrGluLeuGlnGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 101
DB 481 TTCACCTTTTACTGAGCTACAGAAACATAGAAATCAGTGTCATATAATTTCTTAACAT 540
QY 102 LeuGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 121
DB 541 CTAAGAGAAATGATACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 122 TrpAspValLeuPheAlaLeuPheSerGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 141
DB 601 TATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 142 ThrGlnProSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 161
DB 661 ACACACCCAGCAGCTCGATATCTACTGAAATATAATCTGCAATTCGTCGTAAGAAAT 720
QY 162 TrpLeuThrLeuLeuAlaGlyGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 181
DB 721 TGGATACATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 780
QY 182 SerPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 201
DB 781 TCATTTTCAGTTAATGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 202 LeuGlyGlnProGlySerThrAlaValIlePheIleLeuGlnGlySerSerSerSerSer 221
DB 841 CTCACACACCAATATAACACAGCTGTATACCAATATAACACACCAATATAACACACCA 900
QY 222 ArgGlyLeuAspArgSerAlaArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 241
DB 901 CGAGGTACAAACAGAGTGTACAGATATATAACCAATATAACCAATATAACCAATATAAC 960
QY 242 GluValLeuGlyGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 261
DB 961 GAAGTCTCTGTAACACACATGAATGTAATATAGATGAGTCAAAATGCTTTATTTTCAAA 1020
QY 262 AspPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVal 281
DB 1021 AATTTATATATCTTTATGATGATCTCTGACATCTGTAACCAATATAACCAATATAACCA 1080
QY 282 GluAsnLeuSerGlySerGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 301
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QY 302 LeuPheLeuAspHisAspGlyThrLeuGlnThrAspSerSerSerSerSerSerSerSer 321
DB 1141 TTATTTTTCATCATGATAAACTCTTCAGATGATCTATAGACAGTTTTCACACACAG 1200
QY 322 ArgThrProArgGlySerAsnLeuAspGlnGlnValAsnValIleProProIleThrPro 341
DB 1201 ACAACACTATGAGAAATGTAACCTTCATGACAGAGTCAATGTAATTTCCCTCCACACAC 1260
QY 342 ValArgThrValMetAsnThrIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 361
DB 1261 GTTAGGAGCTGTATGACACATGACCAATTAATGATGATGATGATGATGATGATGATGAT 1320

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97	482	TLDELSTYARAYValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaVal	401
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97	642	GluLeuGluHisIleIleTrpThrLeuPheGluHisThrLeuGlnAsuGluTyrGluArg	661
100	2161	GAATTAACAAATATATCTCTCAATCTTTTCTCAACAAACAGCAATATGAACTCT	2220
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Db	2461	AGGCCCCCTACTTGTGCACCAATATCTACATTCCTGAAAGAGCTTAAAGATTTCTTAGT	2520
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RESULT	8		
AAH25755			
Db	AAH25755	standard; DNA; 2995 bp.	
XX	AAH25755;		
XX			
XX			
DT	14-AUG-2001	(first entry)	
XX			
DE	Retinoblastoma tumour suppressor gene.		
XX			
XX	Retinoblastoma; tumour suppressor protein; Rb; p53; cancer;		
KW	adenoviral vector; gene therapy; thymidine kinase; ds		

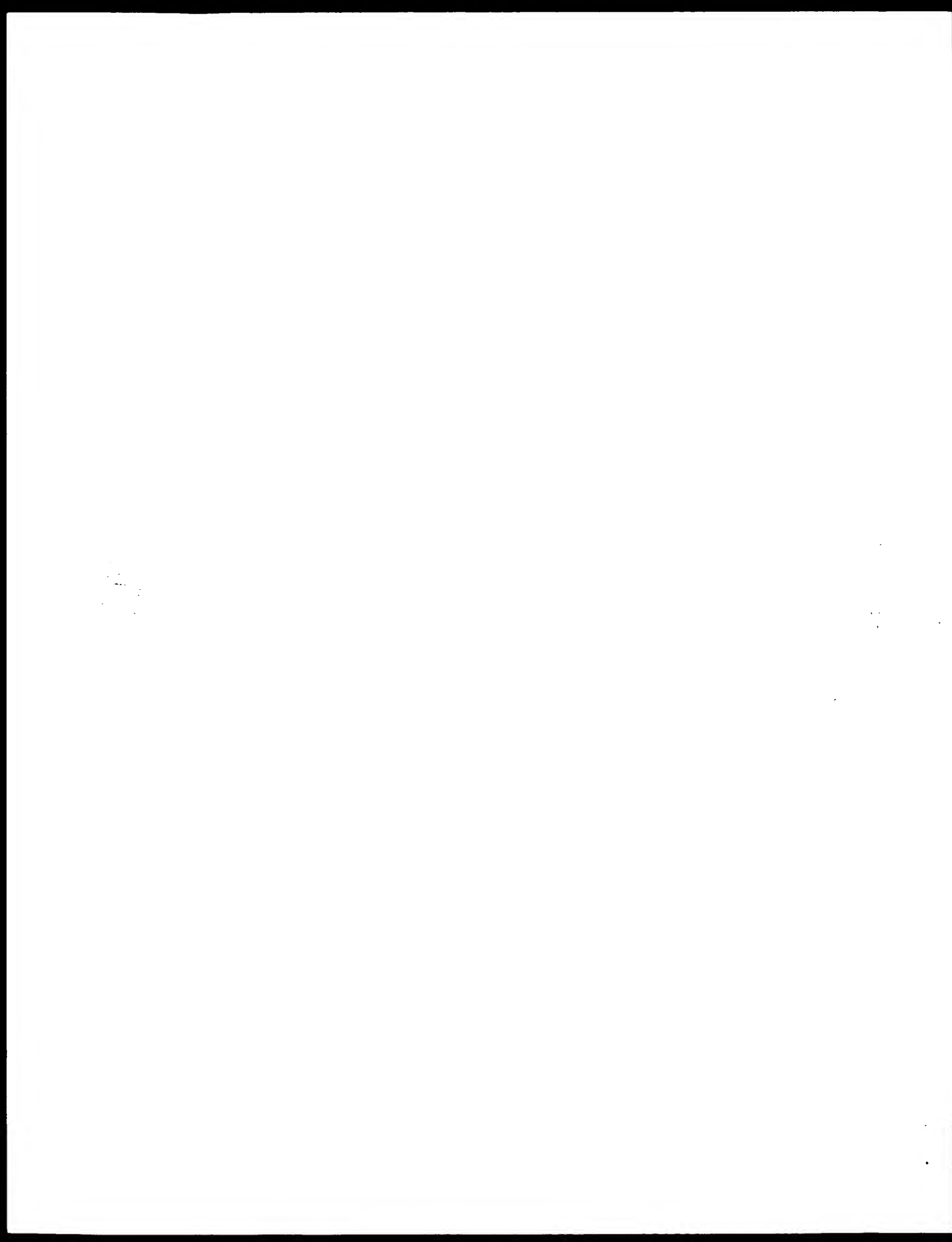
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 44 TTCACCTTTTACTGAGTACACAAAAATATAGAAATCAGTGCATATAATTCCTTAACTTA 540
 45 LeuLysSerGlnIleCysThrSerThrLysValAspAspAlaMetSerAlaLeuLysLys 121
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KW osteosarcoma; fibrosarcoma; glioblastoma; breast cancer;
KW tumorigenesis suppression; SS.
OS Homo sapiens.
PX US9598134-A.
XX 07 DEC-1999.
XX 07 JUN 1995. 9505 0402627.
XX 15-OCT-1987; 8705 0108748.
XX 28 SEP-1992; 9205 0951947.
XX (REGC ) UNIV CALIFORNIA.
PI Lee EYP, Lee W;
XX WP1: 2000-052540/04.
XX p-PSDB; AAY55060.
XX Detecting retinoblastoma gene cancer in mammals
XX Example 6; Fig 7; 34pp; English.
XX This sequence represents the wild type human retinoblastoma gene.
XX The invention relates to a method of detecting a mutated retinoblastoma
XX (mRB) nucleic acid in mammals comprising hybridizing an isolated
XX full-length, wild-type RB (wRB) cDNA probe to a cell sample and
XX detecting a mutated RB nucleic acid. The method is useful as a diagnostic
XX tool for diagnosing retinoblastoma. RB cDNA or genomic DNA are preferably
XX used as probes to determine the defect region of the mRB gene through
XX genomic DNA blotting analysis or using the method of restriction fragment
XX length polymorphism analysis to determine the diseased allele. Cloned RB
XX cDNA can be used to generate specific anti-RB protein (anti pRB110)
XX antibodies which are useful for immunostaining of tissue biopsy. The
XX diagnostic method is particularly intended for use in screening
XX families with a history of hereditary retinoblastoma and for screening
XX their children. It may also be used in prophylactic and postnatal
XX screening and for the prediction of the development of secondary
XX cancer, such as, osteosarcoma, fibrosarcoma, glioblastoma, breast
XX cancer whether or not connected with retinoblastoma. The method is also
XX used in the suppression of tumorigenesis where the absent RB protein
XX pRB110 will be provided through the molecular induction and gene
XX transplanting of the RB cDNA to the individual in need of pRB110.
XX Sequence 2994 RP; 974 A; 618 C; 594 G; 808 T; 0 other;
SQ

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Alignment Scores:

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Pred. No.: 0 Length: 2994
Score: 4797.00 Matches: 928
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Dns: 21 Gaps: 0

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US-09-026-459A-2 (1 928) x AA240287 (1 2994)

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DB 199 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 258
|||||
UY 41 AspLeuProLeuValArgLeuGluThrPheGluThrGluThrArgPheThrAlaLeu 60
|||||
DB 259 GACCTGCTCTCGCTCAGCTTGACCTTGACGAAACAAAGAACTGATTTATGATTA 418
|||||
UY 61 CysGluLysLeuLysIleProAspHisValArgGluArgAlaThrLeuThrIlePheLys 80
|||||
DB 319 TCTCAGAAATTAACATATAGATCATGCTACAGACAGATAGCTTCTCTTAAATCTGCA 478
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RW gene: human; retinoblastoma gene; mutation detection; immunoscreening;
 KW retinoblastoma diagnosis; hereditary retinoblastoma; secondary cancer;


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18 739 GCTAAAGAGAGATACAAATGCAAGATCATCTCGTGGATTTCAGTTAAATGCCA 798
19 221 CysValLeuArgTyrPheLeuLeuLeuSerProPheMetLeuLeuLeuLeuLeuLeu 240
20 749 GGTGCTGCTGCAATATATATTAACAGTCTGACCTCCCAAGTCCGCAAGAACCAIAA 858
21 241 ThrAlaValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 260
22 759 AATATGATACCATTAATGTTTACCTTCACACACCCAGAGAGAGAGAGAGAGAGAG 918
23 241 AlaAlaValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 280
24 769 GATGAGATACCAAAACCACTAGAAAATGATACCAAGAAATTAATCAAGTCTCTGTA 978
25 281 HisLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 300
26 779 CATGAAATGATAATAGATGAGGAGAAAATGTTATTCAAAAATTTATACCTTTATG 1038
27 791 AsnSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 1200
28 1049 AATTCCTTGGACTGTAAATATTAATGAGCTTCCAGAGAGGTTCAGAAATCTTCT 1098
29 321 TyrGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 340
30 1099 TACCAAGAAATATATCTTAAAAATAAAGATCTACATGCAAGATTAATTTGCAIC 1158
31 341 LysThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 360
32 1159 AAAAGAGATGACAGATGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1218
33 361 AsnLeuAspGluGluValAsnValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 380
34 1219 AACCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1278
35 381 ThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 400
36 1279 ACTATGTAACATTAATGATGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1338
37 401 IleSerTyrPheAsnAspCysThrValAsnProLeuLeuLeuLeuLeuLeuLeuLeu 420
38 1339 AATCTGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1398
39 421 AspIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 440
40 1399 GATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1458
41 441 LeuGlySerGlnArgTyrTyrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 460
42 1459 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1518
43 461 LeuLysSerGluGluGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 480
44 1519 GTAAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1578
45 481 IlePheHisMetSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 500
46 1579 AATTTTATATGCTTTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1638
47 501 SerThrSerGlnAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 520
48 1639 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1698
49 521 LeuAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 540
50 1699 GTAAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1758
51 541 AsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 560
52 1759 AATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1818
53 561 LeuAlaThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 580

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1819 CTTCACATGGCTCTCAGATTCACCTTTATTTGATCTTTATTAACAAATCAAAAGAGAGAGAA 1878
19 581 GlyProThrAspHisLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 1900
20 1879 GAGCAATCTATCAGCTGAAATGCTGTTTCTGTAAGATCTCTGTAAGATCTCTGTAAG 1938
21 601 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysLysLysLys 1960
22 1939 ACTGACACATATATGATCTCTCTGTAAGATCTCTGTAAGATCTCTGTAAGATCTCT 1998
23 621 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 2000
24 1999 GGTGTAATTTCTACTGCAATATGCAAGACACAAACCAACCAACCAACCAACCAACCA 2058
25 641 ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeu 2080
26 2059 GATTAAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2118
27 661 ArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIle 2160
28 2119 GAGTAAATACATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2178
29 681 TrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 2200
30 2179 TCGACCTTTCTACCAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2238
31 701 AspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnLeuAspLeu 2260
32 2239 GAGCAATATATGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2298
33 721 PheLysIleLeuValThrAlaTyrLysAspLeuLeuLeuLeuLeuLeuLeuLeuLeu 2320
34 2299 TTTCAATATCTTAAACAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2358
35 741 ArgValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 2380
36 2359 GGTGTTTGTATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2418
37 761 MetGlnArgLeuLysThrAsnIleLeuLeuTyrAlaSerThrArgProProThrLeu 2440
38 2419 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2478
39 781 ProIleProHisIleProArgSerProTyrLysPheTyrSerSerProLeuArgHis 2500
40 2479 GCAATGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2538
41 801 GlyValAsnIleTyrLeuSerProLeuLysSerProTyrLeuLeuLeuLeuLeuLeu 2560
42 2539 GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2598
43 821 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPhe 2620
44 2599 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2658
45 841 ThrSerGlnLysPheGlnLysIleAsnGlnMetValLysAsnSerAspArgValLeu 2680
46 2659 AATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2718
47 861 ArgSerAlaGluLeuLysSerAsnProProLysProLeuLysLysLeuArgPheAsp 2740
48 2719 AGAATGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2778
49 881 GlySerAspGlnAlaAspGlySerLysHisLeuProLysIleSerLysPheGlnLys 2800
50 2779 GATGATATATATATATATATATATATATATATATATATATATATATATATATATAT 2838
51 901 LeuAlaGluMetThrSerThrAlaIleArgMetGlnLysLeuLysMetAspSerMet 2860
52 2839 GTGATCAATATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2898
53 921 AspThrSerAsnLysGlnGluLys 928
54 2899 GATACCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2922

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Search completed: January 18, 2003, 08:14:20
Job time : 432.07 secs

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13 601 GlyProThrAspHisLeuGlySerAlaGlyProLeuAspHisProLeuGlnAsnAsnHis 606
14 602 GlyProThrAspHisLeuGlySerAlaGlyProLeuAspHisProLeuGlnAsnAsnHis 606
15 603 GAGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1938
16 604 ThrAlaAlaAspMetTyrLeuSerProValAlaSerProLysLysLysLysLysLys 620
17 605 ThrAlaAlaAspMetTyrLeuSerProValAlaSerProLysLysLysLysLysLys 620
18 606 ATCTATATATATATATATATATATATATATATATATATATATATATATATATAT 1998
19 607 ArgValAsnSerThrAlaAsnAlaClnIleGlnAlaThrSerAlaIlePheClnThrGlnLys 640
20 608 ArgValAsnSerThrAlaAsnAlaClnIleGlnAlaThrSerAlaIlePheClnThrGlnLys 640
21 609 GCTTAAATTCCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 2058
22 610 ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeu 660
23 611 ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeu 660
24 612 GCAATGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 2118
25 613 ArgLeuAsnThrLeuCysGlnArgLeuLeuSerGlnHisProClnLeuLysLysLysLys 680
26 614 ArgLeuAsnThrLeuCysGlnArgLeuLeuSerGlnHisProClnLeuLysLysLysLys 680
27 615 GGGTAAATATATATATATATATATATATATATATATATATATATATATATATAT 2178
28 616 ArgPheLeuPheGlnHisThrLeuGlnAsnGlnIleTyrClnLeuMetArgAspArgHisLeu 700
29 617 ArgPheLeuPheGlnHisThrLeuGlnAsnGlnIleTyrClnLeuMetArgAspArgHisLeu 700
30 618 TGGAAATTTTGGAAATTTTGGAAATTTTGGAAATTTTGGAAATTTTGGAAATTTTGG 2238
31 619 AsnAlaIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 720
32 620 AsnAlaIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 720
33 621 GATCAAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2298
34 622 PheLysIleIleValThrAlaTyrLysAspLeuProIleAlaValGlnIleThrPheLys 740
35 623 PheLysIleIleValThrAlaTyrLysAspLeuProIleAlaValGlnIleThrPheLys 740
36 624 TTAATAATCATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 2358
37 625 ArgValLeuIleLysGlnGlnIleTyrAspSerIleIleValPheTyrAsnSerValPhe 760
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39 627 GCTATTTTATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2418
40 628 MetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProThrLeuSer 780
41 629 MetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProThrLeuSer 780
42 630 ATGATATATATATATATATATATATATATATATATATATATATATATATATAT 2478
43 631 ProLeuProIleProMetSerProTyrLysPheProSerProLeuArgIlePro 800
44 632 ProLeuProIleProMetSerProTyrLysPheProSerProLeuArgIlePro 800
45 633 GATATATATATATATATATATATATATATATATATATATATATATATATATAT 2538
46 634 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerClnGlnIlePro 820
47 635 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerClnGlnIlePro 820
48 636 GATGAGGAAATATATATATATATATATATATATATATATATATATATATATATAT 2598
49 637 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyLysSerPheGly 840
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51 639 AATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAA 2658
52 640 ThrSerGlnLysPheGlnIleLeuValMetValCysAsnSerArgAlaValLeuLys 860
53 641 ThrSerGlnLysPheGlnIleLeuValMetValCysAsnSerArgAlaValLeuLys 860
54 642 ACTTCGAAAGATTCGAAAGATTCGAAAGATTCGAAAGATTCGAAAGATTCGAAAG 2718
55 643 ArgSerAlaClnGlySerAsnProLysProLeuLysLysLysLysLysLysLysLys 880
56 644 ArgSerAlaClnGlySerAsnProLysProLeuLysLysLysLysLysLysLysLys 880
57 645 AGAATGCTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2778
58 646 GlySerAspGlnAlaAspGlySerLysIleLeuProClnLysSerLysPheClnIleLys 900
59 647 GlySerAspGlnAlaAspGlySerLysIleLeuProClnLysSerLysPheClnIleLys 900
60 648 GCAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2838
61 649 LeuAlaClnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 920
62 650 LeuAlaClnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 920
63 651 CTGATCAAAATGATCTGATCAAAATGATCTGATCAAAATGATCTGATCAAAATGAT 2898
64 652 AspThrSerAsnLysGlnGlnLys 928
65 653 GATATCTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2922
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GenCore version 5.1.3
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09M nucleic acid nucleic search, using sw model

Run on: January 16, 2003, 15:20:17 : Search time 495.71 Seconds
(without alignments)
17541.794 Million cell updates/sec

Database: US 09 026 459a 30

Perfect score: 4392
Sequence: 1 GCGAATACGATTTTATCGT.....AAATGAGCAATATTCATCT 3392

Scoring table: IDENTITY 100
Gapop 10.0, Gapext 1.0

Searches: 2195249 seqs, 1125994159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N_Geneseq_1010922*

Rank	Seq ID	Score	Match	Length	DB ID	Description
1	/S10S2/accataa/geneseq/geneseq-emb1/NA1980.DAT*	4392	100.0	4392	AAV58442	Modified retinoblastoma
2	/S10S2/accataa/geneseq/geneseq-emb1/NA1980.DAT*	4383	99.7	4455	AAV58441	Modified retinoblastoma
3	/S10S2/accataa/geneseq/geneseq-emb1/NA1980.DAT*	4383	99.7	4555	AAV58440	Modified retinoblastoma
4	/S10S2/accataa/geneseq/geneseq-emb1/NA1980.DAT*	4383	99.7	4555	AAV54990	DNA sequence of th
5	/S10S2/accataa/geneseq/geneseq-emb1/NA1980.DAT*	4383	99.7	4849	AAV29391	Human retinoblastoma
6	/S10S2/accataa/geneseq/geneseq-emb1/NA1980.DAT*	4383	99.7	4849	AAV288444	Human androgen rec
7	/S10S2/accataa/geneseq/geneseq-emb1/NA1980.DAT*	4383	99.7	4849	ABU28783	Breast cancer rela
8	/S10S2/accataa/geneseq/geneseq-emb1/NA1980.DAT*	4381.4	99.7	4597	AAU70546	Human retinoblastoma
9	/S10S2/accataa/geneseq/geneseq-emb1/NA1980.DAT*	4381.4	99.7	4597	AAU04501	Human retinoblastoma

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	4392	100.0	4392	AAV58442	Modified retinoblastoma
2	4383	99.7	4455	AAV58441	Modified retinoblastoma
3	4383	99.7	4555	AAV58440	Modified retinoblastoma
4	4383	99.7	4555	AAV54990	DNA sequence of th
5	4383	99.7	4849	AAV29391	Human retinoblastoma
6	4383	99.7	4849	AAV288444	Human androgen rec
7	4383	99.7	4849	ABU28783	Breast cancer rela
8	4381.4	99.7	4597	AAU70546	Human retinoblastoma
9	4381.4	99.7	4597	AAU04501	Human retinoblastoma

Rank	Seq ID	Score	Match	Length	DB ID	Description
10	3379.8	99.6	3554	19	AAV58452	Modified retinoblastoma
11	3379.8	99.6	4597	9	AAV58451	Human retinoblastoma
12	3348.8	98.7	4740	24	ABK86079	Human retinoblastoma
13	3315	97.7	3323	19	AAV58443	Modified retinoblastoma
14	3305.4	97.4	4579	9	AAV58444	Probe for retinoblastoma
15	3257	96.0	3266	19	AAV58445	Modified retinoblastoma
16	3226	95.1	3323	19	AAV58446	Modified retinoblastoma
17	3225.4	95.1	3461	19	AAV58447	Modified retinoblastoma
18	3212	94.7	4238	15	AAV54991	DNA sequence of th
19	3211.4	94.7	4238	15	AAV54992	Modified retinoblastoma
20	3107	91.6	4114	19	AAV58445	Modified retinoblastoma
21	3024.6	89.2	3383	19	AAV58450	Modified retinoblastoma
22	3012.6	88.8	3377	19	AAV58451	Modified retinoblastoma
23	3006	88.6	3447	19	AAV58448	Modified retinoblastoma
24	2945.2	86.8	5056	10	AAV58449	Modified retinoblastoma
25	2827.4	83.4	4161	19	AAV58449	Modified retinoblastoma
26	2691	79.3	2994	11	AAV58449	Cancer suppressor
27	2691	79.3	2994	14	AAV58449	Modified retinoblastoma
28	2691	79.3	2994	19	AAV58449	Modified retinoblastoma
29	2691	79.3	2994	21	AAV58449	Modified retinoblastoma
30	2688	79.2	2995	20	AAV58449	Modified retinoblastoma
31	2688	79.2	2995	20	AAV58449	Modified retinoblastoma
32	2688	79.2	2995	22	AAV58449	Modified retinoblastoma
33	2688	79.2	2995	22	AAV58449	Modified retinoblastoma
34	2688	79.2	2995	23	AAV58449	Modified retinoblastoma
35	2686.4	79.1	2995	16	AAV58449	Modified retinoblastoma
36	2681.6	79.1	2995	16	AAV58449	Modified retinoblastoma
37	835	24.6	18393	20	AAV58449	Modified retinoblastoma
38	841.8	24.5	18177	10	AAV58449	Modified retinoblastoma
39	220.8	6.5	1698	18	AAV58449	Modified retinoblastoma
40	220.8	6.5	1802	18	AAV58449	Modified retinoblastoma
41	220.8	6.5	2331	18	AAV58449	Modified retinoblastoma
42	220.8	6.5	3436	18	AAV58449	Modified retinoblastoma
43	220.8	6.5	4004	18	AAV58449	Modified retinoblastoma
44	218.8	6.5	900	16	AAV58449	Modified retinoblastoma
45	218.8	6.5	1697	16	AAV58449	Modified retinoblastoma

ALIGNMENTS

RESULTS 1
ID AAV58442 standard; DNA: 3392 BP.

XX AAV58442;

XX 02-DEC-1998 (first entry)

DE Modified retinoblastoma tumour suppressor gene.

XX Modified retinoblastoma tumour suppressor gene.

KW Modified retinoblastoma tumour suppressor gene.

FW Human retinoblastoma tumour suppressor gene.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 7..2641

FT /ftaq- a

XX W09837091-A2.

XX 27-AUG-1998.

XX 19-FEB-1998; 98W0-0504041.

XX 20-FEB-1997; 97U5-0048118.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Benedict WF, Hu S, Xu H, Zhou Y.


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DB 1861 AATGACAAATACAGACATATGACAGAGCTTTTCAGCACACCTGACAAATGAGTAT 1920
QY 1921 AATGACAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 1980
DB 1921 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 1980
QY 1981 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2040
DB 1981 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2040
QY 2041 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2100
DB 2041 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2100
QY 2101 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2160
DB 2101 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2160
QY 2161 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2220
DB 2161 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2220
QY 2221 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2280
DB 2221 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2280
QY 2281 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2340
DB 2281 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2340
QY 2341 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2400
DB 2341 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2400
QY 2401 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2460
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QY 2521 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2580
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QY 2581 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2640
DB 2581 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2640
QY 2641 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2700
DB 2641 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2700
QY 2701 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2760
DB 2701 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2760
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DB 2761 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2820
QY 2821 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2880
DB 2821 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2880
QY 2881 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2940
DB 2881 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 2940
QY 2941 AATGACAGAGAGAGAGATTTGAGGACAAATATATGATGTTGACAGTATGATGATG 3000

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DB 2941 GAGTCTGCAIAACGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
QY 3001 GTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060
DB 3001 GTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060
QY 3061 AGAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3120
DB 3061 AGAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3120
QY 3121 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180
DB 3121 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180
QY 3181 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
DB 3181 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
QY 3241 TTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
DB 3241 TTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
QY 3301 ACTGAAACAGATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
DB 3301 ACTGAAACAGATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
QY 3361 ACTGATGCTTTTAAATGAGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420
DB 3361 ACTGATGCTTTTAAATGAGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420

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RESULT 2

AAV58441

ID AAV58441 standard; DNA; 3455 BP.

XX AAV58441;

XX 02-DEC-1998 (first entry)

XX Modified retinoblastoma tumour suppressor gene.

XX Modified retinoblastoma tumour suppressor, K1SP protein; cancer therapy;
cellular proliferation inhibitor; SS.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 7..2694

XX /*cds= a

XX W09837091 A2.

XX 27-AUG-1998.

XX 19-FEB-1998; 98W0-US03041.

XX 20-FEB-1997; 97US-0048118.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX (HXA) UNIV TEXAS SYSTEM.

XX Benedict WF, Hu S, Xu B, Zhou Y;

XX WPI: 1998-480788/41.

XX P-PSDB: AAV69465.

XX retinoblastoma suppressor protein with N terminal modification

XX inhibiting cellular proliferation, particularly cancer

XX Claim 22: Page 142-147, 249pp; English.

XX This sequence encodes a modified retinoblastoma tumour suppressor
protein (K1SP) of the invention. The proteins can be used for inhibiting

cellular proliferation, when coadministered with a p53 protein. The RTSPs can be used for treating diseases characterised by abnormal cellular proliferation, particularly cancers. The RTSPs have a broader spectrum of activity than wild type RTSPs.

SQ Sequence 455 BP: 1153 A; 641 G; 627 G; 1044 T; 0 other;

Query Match 99.7%; Score 3483; DB 19; Length 3455;
 Post local Similarity 100.0%; Pred. No. 0;
 Matches 3383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GATTTTATGTCATTATGTCAGAAATTAAGATACAGATCATGTCAGAGAGAGAGCTGG 69
 DB 74 GATTTTATGTCATTATGTCAGAAATTAAGATACAGATCATGTCAGAGAGAGAGCTGG 132
 QY 70 TTAATTTAGGAGAAATTCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 129
 DB 143 TTAATTTAGGAGAAATTCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 192
 QY 140 AAGAAATTCAG 189
 DB 143 AAGAAATTCAG 252
 QY 140 ACTTTTATGTCAG 249
 DB 253 ACTTTTATGTCAG 312
 QY 250 AAGAAATTCAG 309
 DB 413 AAGAAATTCAG 372
 QY 410 GATGATTTGTTTATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 369
 DB 473 GATGATTTGTTTATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
 QY 470 CAAG 429
 DB 443 CAAG 492
 QY 440 ATCAATTTTATGTCAG 489
 DB 493 ATCAATTTTATGTCAG 552
 QY 490 TTTCAATTTATGTCAG 549
 DB 553 TTTCAATTTATGTCAG 612
 QY 550 AAGAAATTCAG 609
 DB 613 AAGAAATTCAG 672
 QY 610 GTCATACAG 669
 DB 674 GTCATACAG 732
 QY 670 GTTCTCTGTAAGAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729
 DB 734 GTTCTCTGTAAGAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 792
 QY 730 TTTATATTTTATGTCAG 789
 DB 794 TTTATATTTTATGTCAG 852
 QY 790 AATCTCTGTAAGAAATTCAG 849
 DB 854 AATCTCTGTAAGAAATTCAG 912
 QY 850 TTTTGTATCAT 909
 DB 913 TTTTGTATCAT 972
 QY 910 ACAG 969
 DB 974 ACAG 1032

DB 973 ACAG 1022
 QY 970 AG 1029
 DB 1033 AG 1092
 QY 1030 GCTTCAG 1089
 DB 1093 GCTTCAG 1152
 QY 1090 CTGAAAG 1149
 DB 1153 CTGAAAG 1212
 QY 1150 CAGGAG 1209
 DB 1213 CAGGAG 1272
 QY 1210 GTATGAG 1269
 DB 1273 GTATGAG 1332
 QY 1270 CTCTGAG 1329
 DB 1333 CTCTGAG 1392
 QY 1330 GGCAG 1389
 DB 1393 GGCAG 1452
 QY 1390 TGTATGAG 1449
 DB 1453 TGTATGAG 1512
 QY 1450 ATCAAG 1509
 DB 1513 ATCAAG 1572
 QY 1510 CGAG 1569
 DB 1573 CGAG 1632
 QY 1570 TCAAG 1629
 DB 1633 TCAAG 1692
 QY 1630 GTCAG 1689
 DB 1693 GTCAG 1752
 QY 1690 AAG 1749
 DB 1753 AAG 1812
 QY 1750 TCCAG 1809
 DB 1813 TCCAG 1872
 QY 1810 GGCAG 1869
 DB 1873 GGCAG 1932
 QY 1870 TTAAG 1929
 DB 1933 TTAAG 1992
 QY 1930 AG 1989
 DB 1993 AG 2052
 QY 1990 AATATAG 2049
 DB 2053 AATATAG 2112

XX 27 JUN-1994.
 XX 11 AUG-1987; 87EP-0307095.
 XX 11 AUG-1986; 86US-0895163.
 XX (MASS.) MASSACHUSETTS EYE & EAR INFIRMARY.
 XX (MIED.) WHITEHEAD INST BIOMEDICAL RES.
 XX Leyja TP, Friend S;
 XX WJ; 1994 272746/34.
 XX P PSDB; AAR58568.
 XX Inauguring the presence of defective retinoblastoma alleles.
 XX comprises comparing genetic material corresponding to a normal
 XX human retinoblastoma with DNA from a patient.
 XX example 2(2); Figure 7; 18pp; English.
 XX A method for detecting the presence, in a tumour sample, of a protein
 XX the absence of which is associated with a neoplasm, comprises
 XX producing an antibody to the protein and then contacting the
 XX antibody with the tumour sample. Immune complexes indicate the
 XX presence of the protein in the sample. The method may be used in
 XX the detection and treatment of a defective human gene related to
 XX cancer, in particular retinoblastoma.
 XX Sequence 4597 HP; 1489 A; 841 C; 812 G; 1455 T; 0 other;
 XX
 XX Query Match 99.7%; Score 3381.4; DB 15; Length 4597;
 XX Best Local Similarity 100.0%; Field No. 0;
 XX Matches 3382; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 30 CATTTTATTCAGCTATTCAGCAATTAACATACACAGATCATCTCCACAGACAGACTTCG 69
 XX 356 CATTTTATTCAGCTATTCAGCAATTAACATACACAGATCATCTCCACAGACAGACTTCG 225
 XX 70 TTAATTTGGAGAAATTTTCATCTGGATGAGTATTGGAGGTTTATATTTAAAGAAA 129
 XX 226 TTAATTTGGAGAAATTTTCATCTGGATGAGTATTGGAGGTTTATATTTAAAGAAA 285
 XX 330 AAGCAACCTGGGCAATTCATCTATTCAGCAGCAGTTCAGCTACATGACAGATGCTTC 189
 XX 386 AAGCAACCTGGGCAATTCATCTATTCAGCAGCAGTTCAGCTACATGACAGATGCTTC 345
 XX 390 ACCTTTATTCAGCTACAGAAACATAGAAATCAGTGTGCTCAATAATTTCTTAACCTACTA 249
 XX 445 ACCTTTATTCAGCTACAGAAACATAGAAATCAGTGTGCTCAATAATTTCTTAACCTACTA 405
 XX 450 AAGCAACCTGGGCAATTCATCTATTCAGCAGCAGTTCAGCTACATGACAGATGCTTC 404
 XX 406 AAGCAACCTGGGCAATTCATCTATTCAGCAGCAGTTCAGCTACATGACAGATGCTTC 465
 XX 410 GAGGATATTCAGCTACAGAAACATAGAAATCAGTGTGCTCAATAATTTCTTAACCTACTA 369
 XX 456 GAGGATATTCAGCTACAGAAACATAGAAATCAGTGTGCTCAATAATTTCTTAACCTACTA 525
 XX 470 CAATTCAGCTACAGAAACATAGAAATCAGTGTGCTCAATAATTTCTTAACCTACTA 429
 XX 526 CAATTCAGCTACAGAAACATAGAAATCAGTGTGCTCAATAATTTCTTAACCTACTA 585
 XX 430 ATCAATTTTATTCAGCTACAGAAACATAGAAATCAGTGTGCTCAATAATTTCTTAACCTACTA 489
 XX 486 AATCAATTTTATTCAGCTACAGAAACATAGAAATCAGTGTGCTCAATAATTTCTTAACCTACTA 645
 XX 490 TTTCAATTTTATTCAGCTACAGAAACATAGAAATCAGTGTGCTCAATAATTTCTTAACCTACTA 549
 XX 645 TTTCAATTTTATTCAGCTACAGAAACATAGAAATCAGTGTGCTCAATAATTTCTTAACCTACTA 705
 XX 550 AAGCAACCTGGGCAATTCATCTATTCAGCAGCAGTTCAGCTACATGACAGATGCTTC 609

DB 706 AAGCAACCTATATAAAGCAGCTGTTATACCCATTAACCTGATGAGCAATTCAGGCA 765
 QY 610 GGTTCAGCAATAGGAGTGTTCAGGATAGTAAACCAATAGCAAAATATGATTAATGAA 660
 DB 766 GGTTCAGCAATAGGAGTGTTCAGGATAGTAAACCAATAGCAAAATATGATTAATGAA 820
 QY 670 GTTCTCTGTAAAGCAACATGAACTGTAATATAGATGAGCTGCAAAATGTTTATTTCAAAA 720
 DB 826 GTTCTCTGTAAAGCAACATGAACTGTAATATAGATGAGCTGCAAAATGTTTATTTCAAAA 885
 QY 730 TTTATAGCTTTTATGAAATCTCTGAGCTGTATATGCTAAATGAGATGCTGAGGTTGAA 789
 DB 886 TTTATAGCTTTTATGAAATCTCTGAGCTGTATATGCTAAATGAGATGCTGAGGTTGAA 945
 QY 790 AATTTTCTTAAAGCAACATGAACTGTAATATAGATGAGCTGCAAAATGTTTATTTCAAAA 849
 DB 946 AATTTTCTTAAAGCAACATGAACTGTAATATAGATGAGCTGCAAAATGTTTATTTCAAAA 1005
 QY 950 TTTTTCAGCTATGATATAAAGCAGCTGTTATACCCATTAACCTGATGAGCAATTCAGGCA 909
 DB 1006 TTTTTCAGCTATGATATAAAGCAGCTGTTATACCCATTAACCTGATGAGCAATTCAGGCA 1065
 QY 910 AATTTTCTTAAAGCAACATGAACTGTAATATAGATGAGCTGCAAAATGTTTATTTCAAAA 969
 DB 1066 AATTTTCTTAAAGCAACATGAACTGTAATATAGATGAGCTGCAAAATGTTTATTTCAAAA 1125
 QY 970 AAGCACTGTATATAGCAATGAACTGTAATATAGATGAGCTGCAAAATGTTTATTTCAAAA 1029
 DB 1126 AAGCACTGTATATAGCAATGAACTGTAATATAGATGAGCTGCAAAATGTTTATTTCAAAA 1185
 QY 1030 CTTTCAGCAAAATGCTGATTTGCTATTTTAAACATGACAGATGAACTGCAAAATGAAAGTAA 1089
 DB 1186 CTTTCAGCAAAATGCTGATTTGCTATTTTAAACATGACAGATGAACTGCAAAATGAAAGTAA 1245
 QY 1090 CTTTAAAGGCTGAGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1149
 DB 1246 CTTTAAAGGCTGAGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1305
 QY 1150 CTTTAAAGGCTGAGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1209
 DB 1306 CTTTAAAGGCTGAGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1365
 QY 1210 GTTATGCAATTCAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1269
 DB 1366 GTTATGCAATTCAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1425
 QY 1270 CTTTAAAGGCTGAGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1329
 DB 1426 CTTTAAAGGCTGAGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1485
 QY 1330 GTTATGCAATTCAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1389
 DB 1486 GTTATGCAATTCAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1545
 QY 1390 TGGATTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1449
 DB 1546 TGGATTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
 QY 1450 ATCAAGCAACATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1509
 DB 1606 ATCAAGCAACATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1665
 QY 1510 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
 DB 1666 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1725
 QY 1570 TCAAGCAACATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1629
 DB 1726 TCAAGCAACATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1785
 QY 1630 CTTTAAAGGCTGAGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1689
 DB 1786 CTTTAAAGGCTGAGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1845

FR 21 JAN 1988; 8805-0146525.
 FR 23 JAN 1989; 8905-0300667.
 FR 27 SEP 1992; 9205-0951342.
 FR 02 OCT 1992; 9205-0958290.
 XX (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
 FA (WHEAT) WHITEHEAD INST.
 XX 0173a IP; Friend S; Yandell DW;
 XX WPI; 1999-094898/08.
 FR FESDB; AAY01542.
 XX isolated human retinoblastoma gene used to develop products for
 FR analysis predisposition to retinoblastoma and for the detection and
 FR treatment of retinoblastoma
 XX Claim 8; Fig 5; 32pp; English.
 XX This is the nucleic acid sequence of a cDNA of the normal human
 FR retinoblastoma gene Rb. Absence of mutation of the Rb gene (see
 FR also AAX04562) predisposes an individual to retinoblastoma. To
 FR isolate Rb cDNA, the human DNA probe pR3 8, isolated from a human
 FR chromosome 13 lambda phage library, was used in a chromosome walk
 FR to isolate and map 30 kb of genomic DNA surrounding the Rb-R
 FR sequence. Fragment pR30.7R (ATCC 97500) was obtained, and was
 FR used as a probe to screen a cDNA library that had been constructed
 FR from an adenovirus 12 transformed human embryonic retinal cell
 FR line. This provided clone p4.7c (AUG 9784) which in Northern
 FR blots cross-reacted with a 4.7 kb transcript in transformed
 FR retinal cells which was not present in 4 retinoblastoma and one
 FR osteosarcoma cell samples. Rb nucleic acids comprising the Rb
 FR gene cDNA or a fragment of the gene, such as one of the 27 exons
 FR 1-26 introns, can be used in a claimed method for detecting a
 FR deletion or point mutation in the Rb gene of a human patient. The
 FR gene can also be used to synthesize Rb polypeptide (see AAY01542) for
 FR use in the treatment of individuals determined to have a defective
 FR Rb allele.
 XX
 XX Sequence 4597 BP; 1489 A; 841 C; 813 G; 1454 T; 0 other;
 Query Match 99.7%; Score 3381.4; DB 20; Length 4597;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 3382; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GATTTTACTGCATATGCGAAGAAATTAAGATACCAAGATCATCTCAGACAGACAGCTTGG 69
 DB 166 GATTTTATGATATATGATATGATATGATATGATATGATATGATATGATATGATATG 225
 QY 70 TTAACTTGGAGGAAGTTTCATCTGCGAGGAGGATTTGGGAGGTATATATTAAAGGAA 129
 DB 226 TAACTTGGAGGAAGTTTCATCTGCGAGGAGGATTTGGGAGGTATATATTAAAGGAA 285
 QY 136 AAGGAAATGTTGGGGAATTTGATTTTATTTATTTATTTATTTATTTATTTATTTATTT 189
 DB 286 AAGGAAATGTTGGGGAATTTGATTTTATTTATTTATTTATTTATTTATTTATTTATTT 345
 QY 176 ATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 249
 DB 446 ATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 405
 QY 250 AAAAATAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATAT 309
 DB 496 AAAAATAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATAT 465
 QY 410 GATGATATGTTGCTACTCTTACGCAAAATTTGGGAAGGACATGATGAACTTATATATTGACA 369
 DB 466 GATGATATGTTGCTACTCTTACGCAAAATTTGGGAAGGACATGATGAACTTATATATTGACA 525
 QY 470 CAATTCACGACATGACATATCTACTGAAAATAAATTTCCATTGCTGCTTAAAGCTTCTTGG 429
 DB 526 CAATTCACGACATGACATATCTACTGAAAATAAATTTCCATTGCTGCTTAAAGCTTCTTGG 585

QY 430 ATCAGATTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGTGATTTCA 489
 DB 586 ATCAGATTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGTGATTTCA 545
 QY 490 TTTGAGTAAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 549
 DB 646 TTTGAGTAAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
 QY 550 AAAGACCATATAAAGACAGCTGTTATACCCATTAAGGTTACCTTCGGAATATACGATGTA 569
 DB 706 AAAGACCATATAAAGACAGCTGTTATACCCATTAAGGTTACCTTCGGAATATACGATGTA 765
 QY 610 GGTCAAAATAGAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGT 669
 DB 766 GGTCAAAATAGAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGT 825
 QY 670 CTCTCTCTGTAAGACATGCAATGATATATAGAGTATAGAGTATAGAGTATAGAGTAT 729
 DB 826 CTCTCTCTGTAAGACATGCAATGATATATAGAGTATAGAGTATAGAGTATAGAGTAT 885
 QY 730 TTTATATCTTAT 789
 DB 886 TTTATATCTTAT 945
 QY 790 AATCTTTTAAATATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTAT 849
 DB 946 AATCTTTTAAATATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTAT 1005
 QY 850 TTTTGGACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 909
 DB 1006 TTTTGGACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1065
 QY 910 AT 969
 DB 1066 AT 1125
 QY 970 AGAGCTCTTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAG 1029
 DB 1126 AGAGCTCTTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAG 1185
 QY 1030 CTCTCTCTGTAAGACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1089
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 QY 1090 CTGAAAAGAGCTGAGGATATAGGATATAGGATATAGGATATAGGATATAGGATATAG 1149
 DB 1246 CTGAAAAGAGCTGAGGATATAGGATATAGGATATAGGATATAGGATATAGGATATAG 1305
 QY 1150 CAGGCTCTGTAAGACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1209
 DB 1306 CAGGCTCTGTAAGACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1365
 QY 1210 GATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1269
 DB 1366 GATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1425
 QY 1270 CTCTCTGTAAGACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1329
 DB 1426 CTCTCTGTAAGACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1485
 QY 1330 GGCATATATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGT 1389
 DB 1486 GGCATATATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGT 1545
 QY 1390 TGGATCTGATGCTGCTTATTTTAAAGGCTTGGATTTTAAAGGCTTGGATTTTAAAGGCT 1449
 DB 1546 TGGATCTGATGCTTATTTTAAAGGCTTGGATTTTAAAGGCTTGGATTTTAAAGGCTT 1605
 QY 1450 ATCAAGACAGAGGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAG 1509
 DB 1606 ATCAAGACAGAGGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAG 1665
 QY 1510 GGAATATATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTATAGAGTAT 1569

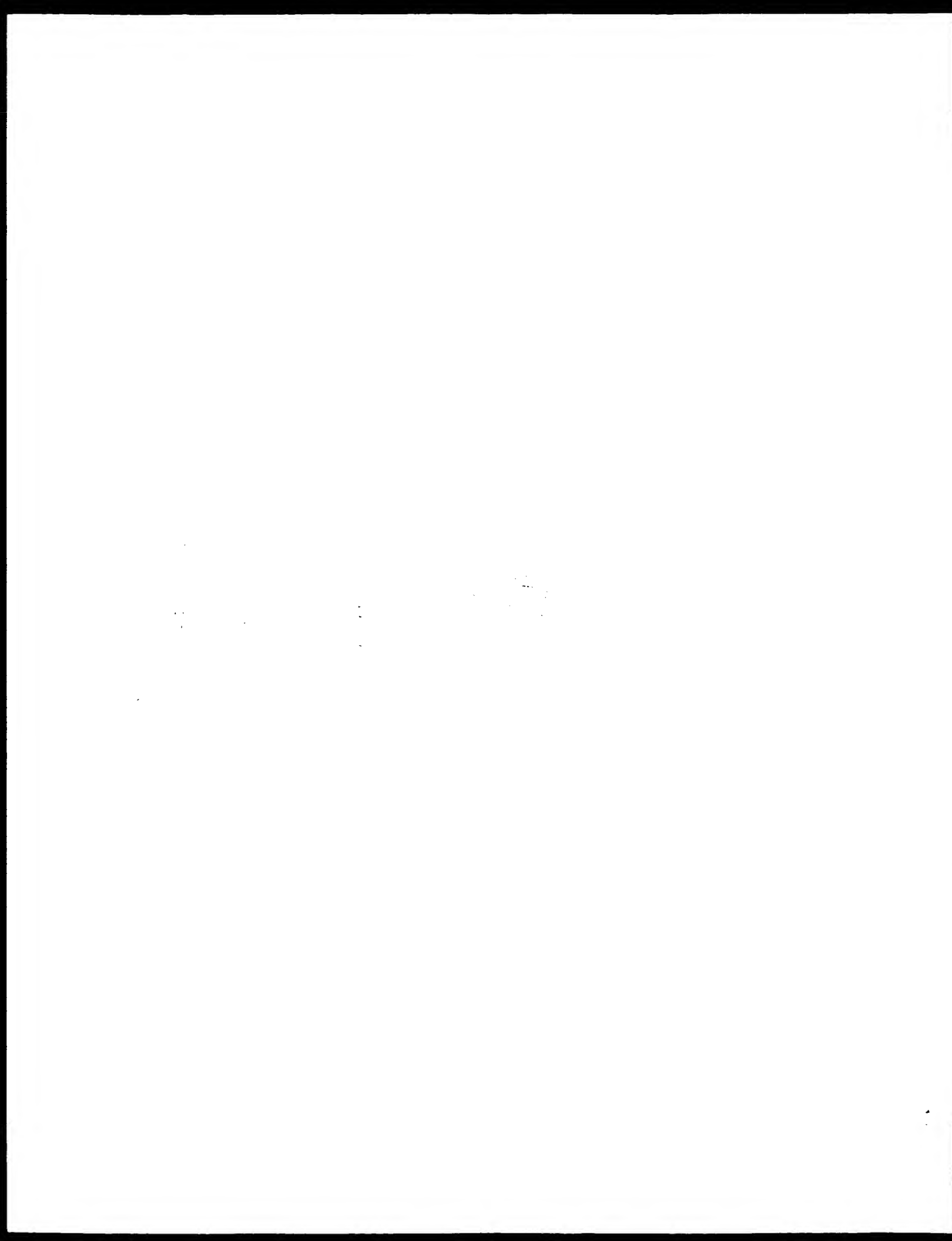
XX W 9847091-A2.
XX
XX 27 AUG-1998.
XX
XX 19 FEB-1998: 98W0-US03041.
XX
XX 20-FEB-1997: 97US-0038118.
XX
XX (BAYL) BAYLOR COLLEGE MEDICINE.
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Medodict WF, Hu S, Xu H, Zhou Y.
XX W21: 1998 468788/41.
XX P-ESCB: AAW9476.
XX
XX retinoblastoma suppressor protein with N-terminal modification -
XX inhibiting cellular proliferation, particularly cancer
XX
XX Claim 22: Page 226-230; 249pp. English.
XX
XX This sequence encodes a modified retinoblastoma tumor suppressor
XX protein (RbSP) of the invention, the proteins can be used for inhibiting
XX cellular proliferation, when coadministered with a p53 protein. The RbSPs
XX can be used for treating diseases characterized by abnormal cellular
XX proliferation, particularly cancers. The RbSPs have a broader spectrum of
XX activity than wild type RbSPs.
XX
XX Sequence 3554 BP; 1170 A; 683 C; 653 G; 1048 T; 0 other;
XX
XX Query March 99.68; Score 3379.8; DB 19; Length 3554;
XX Best Local Similarity 99.98; Pred. No. 0;
XX Matches (incl. conservative) 9; Mismatches 2; Indels 0;
XX
XX 10 GATTTACTGCATTATGTCAGAAATTAACATACACAGATCATGTCAGACAGACAGCTTGG 69
XX
XX 172 GATTTACTGCATTATGTCAGAAATTAACATACACAGATCATGTCAGACAGACAGCTTGG 231
XX
XX 70 TTAAGTGGAGAAATTTTCATCTGTGGATGGAGTATTTGGAGGTTATATTCAGAAAGAAA 129
XX
XX 242 TTAACATGGAGAAATTTTCATCTGTGGATGGAGTATTTGGAGGTTATATTCAGAAAGAAA 291
XX
XX 340 AAGGAAATGGTGGGAAATTCATCTGTGGATGGAGTATTTGGAGGTTATATTCAGAAAGAAA 369
XX
XX 292 AAGGAAATGGTGGGAAATTCATCTGTGGATGGAGTATTTGGAGGTTATATTCAGAAAGAAA 351
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XX 340 AATTTTAACTGAGCTATACAGAAAGAAATAGAAATCAGTGTGGATTTAACTTACCTAC 249
XX
XX 352 AATTTTAACTGAGCTATACAGAAAGAAATAGAAATCAGTGTGGATTTAACTTACCTAC 411
XX
XX 250 AAAAATAATGATACAGTACCAAGATTTGATATGCTATGTCAGAGTGTGTGAGAAAGATAT 309
XX
XX 412 AAGGAAATGGTGGGAAATTTTCATCTGTGGATGGAGTATTTGGAGGTTATATTCAGAAAG 471
XX
XX 340 AATTTTAACTGAGCTATACAGAAAGAAATAGAAATCAGTGTGGATTTAACTTACCTAC 369
XX
XX 472 GATGATGTTGTCATCT 531
XX
XX 470 CAAGCCAGGAGTTCGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 429
XX
XX 542 CAAGCCAGGAGTTCGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 591
XX
XX 440 ATACATTTTATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 489
XX
XX 592 ATACATTTTATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 651
XX
XX 490 TTTCAATTTATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 549
XX
XX 452 TTTCAATTTATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 711
XX
XX 550 AAGGAAATGGTGGGAAATTTTCATCTGTGGATGGAGTATTTGGAGGTTATATTCAGAAAGAAA 609
XX
XX
XX

DB 712 AAGAACCAATATAAAGACAGCTGTTATACCCATTAAGGTTACCCGGAACATCCAGGCA 771
QY
DB 610 GATTCAGAAATAGAGAGTGTGATAGTAAAGCAATAGAGAAATGATACAGAAATATTGAA 669
DB 772 GATTCAGAAATAGAGAGTGTGATAGTAAAGCAATAGAGAAATGATACAGAAATATTGAA 841
QY
DB 670 GATTCAGTAAAGCAATAGAGTAAATAGAGAGTGTGATAGTAAAGCAATAGAGAAATATTGAA 729
DB 832 GATTCAGTAAAGCAATAGAGTAAATAGAGAGTGTGATAGTAAAGCAATAGAGAAATATTGAA 892
QY
DB 730 TTTATAGCTTTTATGAAATCTCTGAGTGTGATAGTAAAGCAATAGAGAAATATTGAA 784
DB 892 TTTATAGCTTTTATGAAATCTCTGAGTGTGATAGTAAAGCAATAGAGAAATATTGAA 951
QY
DB 790 AATCTTTCTAAAGCAGTACAGAGAAATTTATCTTAAAGCAATAGAGAAATATTGAA 849
DB 952 AATCTTTCTAAAGCAGTACAGAGAAATTTATCTTAAAGCAATAGAGAAATATTGAA 1011
QY
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DB 1012 TTTTGGATCATGATAAAGCAATAGAGTAAATAGAGAGTGTGATAGTAAAGCAATAGAGAA 1071
QY
DB 910 ACAGCAGGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 969
DB 1072 ACAGCAGGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1131
QY
DB 970 AGAGCTTTTATGAAATCTCTGAGTGTGATAGTAAAGCAATAGAGAAATATTGAA 1029
DB 1132 AGAGCTTTTATGAAATCTCTGAGTGTGATAGTAAAGCAATAGAGAAATATTGAA 1191
QY
DB 1030 CTTTCAGAAATCTGATTTCTTATTTTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAG 1089
DB 1192 CTTTCAGAAATCTGATTTCTTATTTTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAG 1251
QY
DB 1090 CTGAAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1149
DB 1252 CTGAAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1311
QY
DB 1150 CAGAGCTTTTATGAAATCTCTGAGTGTGATAGTAAAGCAATAGAGAAATATTGAA 1209
DB 1312 CAGAGCTTTTATGAAATCTCTGAGTGTGATAGTAAAGCAATAGAGAAATATTGAA 1371
QY
DB 1210 GTATTCAGTAAATCTGATTTCTTATTTTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAG 1269
DB 1372 GTATTCAGTAAATCTGATTTCTTATTTTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAG 1431
QY
DB 1270 CTTTCAGTAAATCTGATTTCTTATTTTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAG 1329
DB 1432 CTTTCAGTAAATCTGATTTCTTATTTTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAG 1491
QY
DB 1330 GGTATATAGTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1389
DB 1492 GGTATATAGTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1551
QY
DB 1390 TGTATTCAGTAAATCTGATTTCTTATTTTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1449
DB 1552 TGTATTCAGTAAATCTGATTTCTTATTTTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1611
QY
DB 1450 ATCAAGAGTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1509
DB 1612 ATCAAGAGTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1671
QY
DB 1510 GGTATATAGTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1569
DB 1672 GGTATATAGTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1731
QY
DB 1570 TCAAGAGCAGTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1629
DB 1732 TCAAGAGTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1791
QY
DB 1630 CTGAAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1689
DB 1792 CTGAAAGAGTAAAGCAATAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1851

XX Sequence 3324 bp: 1114 A; 605 G; 591 C; 1013 T; 0 other;
 Query Match: 97.7%; Score 3315; DB 19; Length 3323;
 Best Local Similarity 100 nks; Pred No 0;
 Matches 3315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 78 GATGAAAATTTTCATCTGCTGATGATCAATATGGCAGGTATATATTCACAAAGAAAAAGCAACT 137
 14 9 GAGAAATTTTCATCTGCTGATGATGATCAATATGGCAGGTATATATTCACAAAGAAAAAGCAACT 68
 27 148 GGGGAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 197
 14 24 GGGGAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 128
 27 148 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 257
 14 124 TGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 188
 27 248 GAT 317
 14 148 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 248
 27 318 GAT 377
 14 249 GAT 308
 27 437 GAT 437
 14 368 GAT 368
 27 497 GAT 497
 14 428 GAT 428
 27 557 GAT 557
 14 488 GAT 488
 27 617 GAT 617
 14 548 GAT 548
 27 677 GAT 677
 14 608 GAT 608
 27 737 GAT 737
 14 668 GAT 668
 27 797 GAT 797
 14 728 GAT 728
 27 857 GAT 857
 14 788 GAT 788
 27 917 GAT 917
 14 848 GAT 848
 27 977 GAT 977
 14 908 GAT 908
 27 1037 GAT 1037
 14 968 GAT 968
 27 1097 GAT 1097

Db 969 AAAATCAGATTTGCTATTTTAAACAATCCACAGTGAATTCACAAAGAAAGATATATTCACAAAG 1028
 QY 1098 AGTGAAGGATATAGGATACATCTTTTAAAGAGAAATTTGCTAAAGCTGTGGGAAAGAGTTG 1157
 Db 1029 AGTGAAGGATATAGGATACATCTTTTAAAGAGAAATTTGCTAAAGCTGTGGGAAAGAGTTG 1088
 QY 1158 TGTGGAATTCAGATTCACAGTATACAAATTCAGAGTTCGCTTCTATATACCAAGTAAATCA 1217
 Db 1089 TGTGGAATTCAGATTCACAGTATACAAATTCAGAGTTCGCTTCTATATACCAAGTAAATCA 1148
 QY 1218 ATGATGCTTTAAATCAGAGAGAGAGATATATCATTCAAAATTTTATGCAAAATTTTGTGAA 1277
 Db 1149 ATGATGCTTTAAATCAGAGAGAGAGATATATCATTCAAAATTTTATGCAAAATTTTGTGAA 1208
 QY 1278 TGAATATTTTATATATGTTTATATATGTTTATATATATATATATATATATATATATATATAT 1347
 Db 1209 TGAATATTTTATATATGTTTATATATGTTTATATATATATATATATATATATATATATATAT 1268
 QY 1338 TACAT 1397
 Db 1269 TAT 1328
 QY 1398 GAATGCTTTAAATTTAAAT 1457
 Db 1329 GAATGCTTTAAATTTAAAT 1388
 QY 1458 ATGATGCTTTAAATTTAAAT 1517
 Db 1389 ATGATGCTTTAAATTTAAAT 1448
 QY 1518 GGAATGCTTTAAATTTAAAT 1577
 Db 1449 GGAATGCTTTAAATTTAAAT 1508
 QY 1578 ATGATGCTTTAAATTTAAAT 1637
 Db 1509 ATGATGCTTTAAATTTAAAT 1568
 QY 1638 TAT 1697
 Db 1569 TAT 1628
 QY 1698 ATGATGCTTTAAATTTAAAT 1757
 Db 1629 ATGATGCTTTAAATTTAAAT 1688
 QY 1758 ATGATGCTTTAAATTTAAAT 1817
 Db 1689 ATGATGCTTTAAATTTAAAT 1748
 QY 1818 ATGATGCTTTAAATTTAAAT 1877
 Db 1749 ATGATGCTTTAAATTTAAAT 1808
 QY 1878 ATGATGCTTTAAATTTAAAT 1937
 Db 1809 ATGATGCTTTAAATTTAAAT 1868
 QY 1938 ATGATGCTTTAAATTTAAAT 1997
 Db 1869 ATGATGCTTTAAATTTAAAT 1928
 QY 1998 ATGATGCTTTAAATTTAAAT 2057
 Db 1929 ATGATGCTTTAAATTTAAAT 1988
 QY 2058 ATGATGCTTTAAATTTAAAT 2117
 Db 1989 ATGATGCTTTAAATTTAAAT 2048
 QY 2118 ATGATGCTTTAAATTTAAAT 2177
 Db 2049 ATGATGCTTTAAATTTAAAT 2108



Genome version 5.1.3
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M nucleotide nucleotide search, using SW model

Run on: January 16, 2003, 15:20:17 : Search time 444.802 Seconds
(without alignments)
17541.794 Million cell updates/sec

Files: US 09 026 459A 28
Percent score: 44.5
Sequence: 1 GCGTATGAGAGAAACGGG.....AAATGASAAATATGATG 4455

Scoring table: Identity: 100
Gap: 16.0 : Gap: 1.0

Searched: 245249 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum hit seq length: 3
Maximum hit seq length: 2000000
Post processing: Minimum Match 6X
Maximum Match 100X
List first 45 summaries

Database	N	Genes	101002	*
1	1	US09026459A	28	US09026459A
2	2	US09026459A	28	US09026459A
3	3	US09026459A	28	US09026459A
4	4	US09026459A	28	US09026459A
5	5	US09026459A	28	US09026459A
6	6	US09026459A	28	US09026459A
7	7	US09026459A	28	US09026459A
8	8	US09026459A	28	US09026459A
9	9	US09026459A	28	US09026459A
10	10	US09026459A	28	US09026459A
11	11	US09026459A	28	US09026459A
12	12	US09026459A	28	US09026459A
13	13	US09026459A	28	US09026459A
14	14	US09026459A	28	US09026459A
15	15	US09026459A	28	US09026459A
16	16	US09026459A	28	US09026459A
17	17	US09026459A	28	US09026459A
18	18	US09026459A	28	US09026459A
19	19	US09026459A	28	US09026459A
20	20	US09026459A	28	US09026459A
21	21	US09026459A	28	US09026459A
22	22	US09026459A	28	US09026459A
23	23	US09026459A	28	US09026459A
24	24	US09026459A	28	US09026459A

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Prod. No.	Score	Query	Match	Length	DB	ID	Description
1	44.5	100.0	44.5	19	AAV58441		Modified retinoblastoma
2	44.7	99.8	45.5	19	AAV58440		Modified retinoblastoma
3	44.7	99.8	45.5	19	AAV54930		DNA sequence of the
4	44.7	99.8	44.9	21	AAV29391		Human retinoblastoma
5	44.7	99.8	44.9	21	AAV28444		Human androgen receptor
6	44.7	99.8	44.9	24	AAV2873		Breast cancer related
7	44.4	99.4	45.4	19	AAV58452		Modified retinoblastoma
8	44.4	99.4	45.4	19	AAV70536		Human retinoblastoma
9	44.4	99.4	45.4	20	AAV04501		Human retinoblastoma

Human retinoblastoma
Human retinoblastoma
Modified retinoblastoma
Probe for retinoblastoma
Modified retinoblastoma
Modified retinoblastoma
Modified retinoblastoma
Modified retinoblastoma
DNA sequence of the
Retinoblastoma 44K
Modified retinoblastoma
Modified retinoblastoma
Modified retinoblastoma
Modified retinoblastoma
DNA of human retinoblastoma
Modified retinoblastoma
Cancer suppressor
Retinoblastoma gene
Retinoblastoma protein
K12 type human retinoblastoma
Human p10-RB retinoblastoma
cDNA encoding a retinoblastoma protein
Retinoblastoma tumor
Retinoblastoma tumor
Retinoblastoma tumor
Retinoblastoma tumor
Human Rb10 cDNA
DNA of human retinoblastoma
Antisense sequence
Direct tandem repeat
Construct pMK10/AS
Construct pMK10/AS
Construct pMK10/AS
Construct pMK10/AS
Retinoblastoma protein
Retinoblastoma protein

ALIGNMENTS

RESULT 1

AAV58441 standard; DNA: 4455 BP.

AAV58441:

AAV58441: 19 FEB 1998 (first entry)

Modified retinoblastoma tumor suppressor gene.

Modified retinoblastoma tumor suppressor, RbSP protein, cancer therapy, cellular proliferation inhibitor; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 7..2694

W09837091-A2.

27-AUG-1998.

19-FEB-1998; 98W0-US04041.

20-FEB-1997; 97US-0048118.

(HAYU) BAYLOR COLLEGE MEDICINE.

(TEXA) UNIV TEXAS SYSTEM.

Benedict WF, Hu S, Xu H, Zhou Y.

